Figure 1

GATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACATTTTGGAAGACAGTATTCAGAAAAAAAATTTCC
TTAATAAAAATACAACTCAGATCCTTCAAATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTATTTTCTTCTTTGTTTTC
TTGCTACGTATAATTATTAATATCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTTACCATGCAGTCCAAATCTAAAC
TGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACAGCAAAGGAA
AATAAACACAGAATATAATAAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTTTAGAACTCCCAACCACATTTGGATC

FIG. 2A

```
             9           18           27           36           45           54
5' CAG AGA GGC TGT ATT TCA GTG CAG CCT GCC AGA CCT CTT CTG GAG GAA GAC TGG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

            63           72           81           90           99          108
   ACA AAG GGG GTC ACA CAT TCC TTC CAT ACG GTT GAG CCT CTA CCT GCC TGG TGC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

           117          126          135          144          153          162
   TGG TCA CAG TTC AGC TTC TTC ATG ATG GTG GAT CCC AAT GGC AAT GAA TCC AGT
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
                                M   M   V   D   P   N   G   N   E   S   S

           171          180          189          198          207          216
   GCT ACA TAC TTC ATC CTA ATA GGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    A   T   Y   F   I   L   I   G   L   P   G   L   E   E   A   Q   F   W

           225          234          243          252          261          270
   TTG GCC TTC CCA TTG TGC TCC CTC TAC CTT ATT GCT GTG CTA GGT AAC TTG ACA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L   A   F   P   L   C   S   L   Y   L   I   A   V   L   G   N   L   T

           279          288          297          306          315          324
   ATC ATC TAC ATT GTG CGG ACT GAG CAC AGC CTG CAT GAG CCC ATG TAT ATA TTT
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    I   I   Y   I   V   R   T   E   H   S   L   H   E   P   M   Y   I   F

           333          342          351          360          369          378
   CTT TGC ATG CTT TCA GGC ATT GAC ATC CTC ATC TCC ACC TCA TCC ATG CCC AAA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L   C   M   L   S   G   I   D   I   L   I   S   T   S   S   M   P   K

           387          396          405          414          423          432
   ATG CTG GCC ATC TTC TGG TTC AAT TCC ACT ACC ATC CAG TTT GAT GCT TGT CTG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    M   L   A   I   F   W   F   N   S   T   T   I   Q   F   D   A   C   L

           441          450          459          468          477          486
   CTA CAG ATT TTT GCC ATC CAC TCC TTA TCT GGC ATG GAA TCC ACA GTG CTG CTG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L   Q   I   F   A   I   H   S   L   S   G   M   E   S   T   V   L   L

           495          504          513          522          531          540
   GCC ATG GCT TTT GAC CGC TAT GTG GCC ATC TGT CAC CCA CTG CGC CAT GCC ACA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    A   M   A   F   D   R   Y   V   A   I   C   H   P   L   R   H   A   T

           549          558          567          576          585          594
   GTA CTT ACG TTG CCT CGT GTC ACC AAA ATT GGT GTG GCT GCT GTG GTG CGG GGG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V   L   T   L   P   R   V   T   K   I   G   V   A   A   V   V   R   G

           603          612          621          630          639          648
   GCT GCA CTG ATG GCA CCC CTT CCT GTC TTC ATC AAG CAG CTG CCC TTC TGC CGC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    A   A   L   M   A   P   L   P   V   F   I   K   Q   L   P   F   C   R
```

FIG. 2B

```
        657         666         675         684         693         702
TCC AAT ATC CTT TCC CAT TCC TAC TGC CTA CAC CAA GAT GTC ATG AAG CTG GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   N   I   L   S   H   S   Y   C   L   H   Q   D   V   M   K   L   A

        711         720         729         738         747         756
TGT GAT GAT ATC CGG GTC AAT GTC GTC TAT GGC CTT ATC GTC ATC ATC TCC GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   D   D   I   R   V   N   V   V   Y   G   L   I   V   I   I   S   A

        765         774         783         792         801         810
ATT GGC CTG GAC TCA CTT CTC ATC TCC TTC TCA TAT CTG CTT ATT CTT AAG ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   G   L   D   S   L   L   I   S   F   S   Y   L   L   I   L   K   T

        819         828         837         846         855         864
GTG TTG GGC TTG ACA CGT GAA GCC CAG GCC AAG GCA TTT GGC ACT TGC GTC TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   L   G   L   T   R   E   A   Q   A   K   A   F   G   T   C   V   S

        873         882         891         900         909         918
CAT GTG TGT GCT GTG TTC ATA TTC TAT GTA CCT TTC ATT GGA TTG TCC ATG GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   V   C   A   V   F   I   F   Y   V   P   F   I   G   L   S   M   V

        927         936         945         954         963         972
CAT CGC TTT AGC AAG CGG CGT GAC TCT CCG CTG CCC GTC ATC TTG GCC AAT ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   R   F   S   K   R   R   D   S   P   L   P   V   I   L   A   N   I

        981         990         999        1008        1017        1026
TAT CTG CTG GTT CCT CCT GTG CTC AAC CCA ATT GTC TAT GGA GTG AAG ACA AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   L   L   V   P   P   V   L   N   P   I   V   Y   G   V   K   T   K

       1035        1044        1053        1062        1071        1080
GAG ATT CGA CAG CGC ATC CTT CGA CTT TTC CAT GTG GCC ACA CAC GCT TCA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   I   R   Q   R   I   L   R   L   F   H   V   A   T   H   A   S   E

       1089        1098        1107        1116        1125        1134
CCC TAG GTG TCA GTG ATC AAA CTT CTT TTC CAT TCA GAG TCC TCT GAT TCA GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   *

       1143        1152        1161        1170        1179        1188
TTT AAT GTT AAC ATT TTG GAA GAC AGT ATT CAG AAA AAA AAT TTC CTT AAT AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1197        1206        1215        1224        1233        1242
AAA TAC AAC TCA GAT CCT TCA AAT ATG AAA CTG GTT GGG GAA TCT CCA TTT TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1251        1260        1269        1278        1287        1296
CAA TAT TAT TTT CTT CTT TGT TTT CTT GCT ACA TAT AAT TAT TAA TAC CCT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1305        1314        1323        1332        1341        1350
TAG GTT GTG GTT GGA GGG TTA TTA CTT TTC ATT TTA CCA TGC AGT CCA AAT CTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
```

FIG. 2C

```
  1359        1368        1377        1386        1395        1404
AAC TGC TTC TAC TGA TGG TTT ACA GCA TTC TGA GAT AAG AAT GGT ACA TCT AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1413        1422        1431        1440        1449        1458
GAA CAT TTG CCA AAG GCC TAA GCA CGG CAA AGG AAA ATA AAC ACA GAA TAT AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1467        1476        1485        1494        1503        1512
AAA ATG AGA TAA TCT AGC TTA AAA CTA TAA CTT CCT CTT CAG AAC TCC CAA CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1521        1530        1539        1548        1557        1566
CAT TGG ATC TCA GAA AAA TGC TGT CTT CAA AAT GAC TTC TAC AGA GAA GAA ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1575        1584        1593        1602        1611        1620
ATT TTT CCT CTG GAC ACT AGC ACT TAA GGG GAA GAT TGG AAG TAA AGC CTT GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1629        1638        1647        1656        1665        1674
AAG AGT ACA TTT ACC TAC GTT AAT GAA AGT TGA CAC ACT GTT CTG AGA GTT TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1683        1692        1701        1710        1719        1728
ACA GCA TAT GGA CCC TGT TTT TCC TAT TTA ATT TTC TTA TCA ACC CTT TAA TTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1737        1746        1755        1764        1773        1782
GGC AAA GAT ATT ATT AGT ACC CTC ATT GTA GCC ATG GGA AAA TTG ATG TTC AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1791        1800        1809        1818        1827        1836
GGG GAT CAG TGA ATT AAA TGG GGT CAT ACA AGT ATA AAA ATT AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1845        1854        1863        1872        1881        1890
GAC TTC ATG CCC AAT CTC ATA TGA TGT GGA AGA ACT GTT AGA GAG ACC AAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1899        1908        1917        1926        1935        1944
GTA GTG GGT TAG AGA TTT CCA GAG TCT TAC ATT TTC TAG AGG AGG TAT TTA ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        1953        1962        1971        1980        1989        1998
TCT TCT CAC TCA TCC AGT GTT GTA TTT AGG AAT TTC CTG GCA ACA GAA CTC ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2007        2016        2025        2034        2043        2052
GCT TTA ATC CCA CTA GCT ATT GCT TAT TGT CCT GGT CCA ATT GCC AAT TAC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2061        2070        2079        2088        2097        2106
TGT CTT GGA AGA AGT GAT TTC TAG GTT CAC CAT TAT GGA AGA TTC TTA TTC AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2115        2124        2133        2142        2151        2160
AAG TCT GCA TAG GGC TTA TAG CAA GTT ATT TAT TTT TAA AAG TTC CAT AGG TGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2169        2178        2187        2196        2205        2214
TTC TGA TAG GCA GTG AGG TTA GGG AGC CAC CAG TTA TGA TGG GAA GTA TGG AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2223        2232        2241        2250        2259        2268
GGC AGG TCT TGA AGA TAA CAT TGG CCT TTT GAG TGT GAC TCG TAG CTG GAA AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2277        2286        2295        2304        2313        2322
GAG GGA ATC TTC AGG ACC ATG CTT TAT TTG GGG CTT TGT GCA GTA TGG AAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2331        2340        2349        2358        2367        2376
GAC TTT GAG ACC AGG AAA GCA ATC TGA CTT AGG CAT GGG AAT CAG GCA TTT TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
```

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FIG. 2D

```
    2385        2394        2403        2412        2421        2430
CTT CTG AGG GGC TAT TAC CAA GGG TTA ATA GGT TTC ATC TTC AAC AGG ATA TGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2439        2448        2457        2466        2475        2484
CAA CAG TGT TAA CCA AGA AAC TCA AAT TAC AAA TAC TAA AAC ATG TGA TCA TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2493        2502        2511        2520        2529        2538
ATG TGG TAA GTT TCA TTT TCT TTT TCA ATC CTC AGG TTC CCT GAT ATG GAT TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2547        2556        2565        2574        2583        2592
TAT AAC ATG CTT TCA TCC CCT TTT GTA ATG GAT ATC ATA TTT GGA AAT GCC TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2601        2610        2619        2628        2637        2646
TTA ATA CTT GTA TTT GCT GCT GGA CTG TAA GCC CAT GAG GGC ACT GTT TAT TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2655        2664        2673        2682        2691        2700
TGA ATG TCA TCT CTG TTC ATC ATT GAC TGC TCT TTG CTC ATC ATT GAA TCC CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2709        2718        2727        2736        2745        2754
AGC AAA GTG CCT AGA ACA TAA TAG TGC TTA TGC TTG ACA CCG GTT ATT TTT CAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2763        2772        2781        2790        2799        2808
CAA ACC TGA TTC CTT CTG TCC TGA ACA CAT AGC CAG GCA ATT TTC CAG CCT TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2817        2826        2835        2844        2853        2862
TTG AGT TGG GTA TTA TTA AAT TCT GGC CAT TAC TTC CAA TGT GAG TGG AAG TGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2871        2880        2889        2898        2907        2916
CAT GTG CAA TTT CTA TAC CTG GCT CAT AAA ACC CTC CCA TGT GCA GCC TTT CAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2925        2934        2943        2952        2961        2970
GTT GAC ATT AAA TGT GAC TTG GGA AGC TAT GTG TTA CAC AGA GTA AAT CAC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        2979        2988        2997        3006        3015        3024
AAG CCT GGA TTT CTG AAA AAA CTG TGC AGA GCC AAA CCT CTG TCA TTT GCA ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        3033        3042        3051        3060        3069        3078
CCC ACT TGT ATT TGT ACG AGG CAG TTG GAT AAG TGA AAA ATA AAG TAC TAT TGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
        3087        3096        3105        3114        3123        3132
GTC AAG AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

AAA A 3'
--- -
```

Figure 3: Protein Sequence for 101P3A11.

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILI
STSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPRVTKIGV
AAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYL
LILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYG
VKTKEIRQRILRLFHVATHASEP

Figure 4

Alignment of 101P3A11 (Sbjct) with mouse olfactory receptor S25 (Query)

```
Query: 34  GNYTVVTEFILLGLTDDITVSVILFVMFLIVYSVTLMGNLNIIVLIRTSPQLHTPMYLFL 93
           GN +  T FIL+GL         L      +Y + ++GNL II ++RT   LH PMY+FL
Sbjct: 6   GNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL 65

Query: 94  SHLAFLDIGYSSSVTPIMLRGFLRKGTFIPVAGCVAQLCIVVAFGTSESFLLASMAYDRY 153
             L+ +DI  S+S  P ML  F    T I    C+ Q+  + +    ES +L +MA+DRY
Sbjct: 66  CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRY 125

Query: 154 VAICSPLLYSTQMSSTVCILLVGTSYLGGWVNAWIFTGCSLNLSFCGPNKINHFFCDYSP 213
           VAIC PL ++T ++      +   + + G             L FC  N ++H +C +
Sbjct: 126 VAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQD 185

Query: 214 LLKLSCSHDFSFEVIPAISSGSIIVVTVFIIALSYVYILVSILKMRSTEGRQKAFSTCTS 273
           ++KL+C       V   I   S I +   +I+ SY+ IL ++L + + E + KAF TC S
Sbjct: 186 VMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244

Query: 274 HLTAVTLFFGTITFIYVMPQSSYSTDQNK----VVSVFYTVVIPMLNPLIYSFRNKEVKE 329
           H+ AV +F+  + FI +     +S  ++     +++  Y +V P+LNP++Y  + KE+++
Sbjct: 245 HVCAVFIFY--VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQ 302

Query: 330 AMKKL 334
            + +L
Sbjct: 303 RILRL 307
```

Figure 5:
101P3A11 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

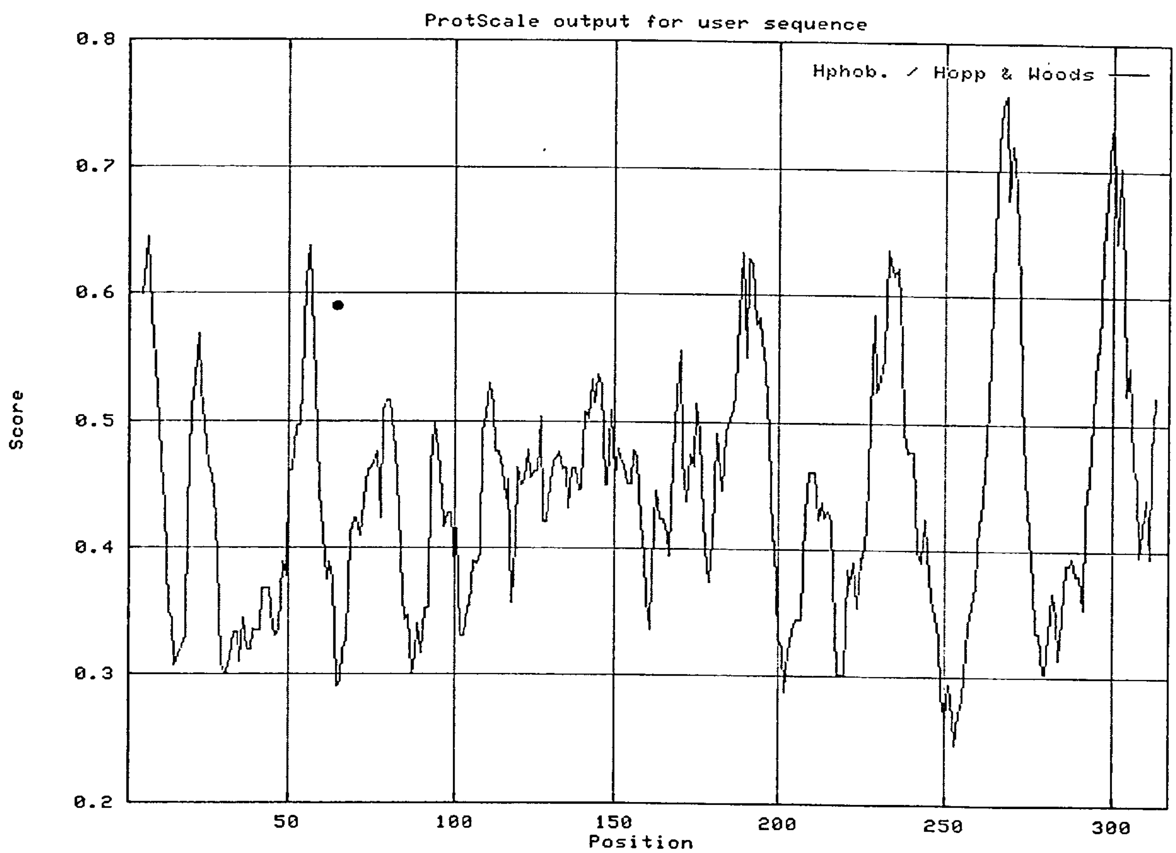

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Figure 6:
101P3A11 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

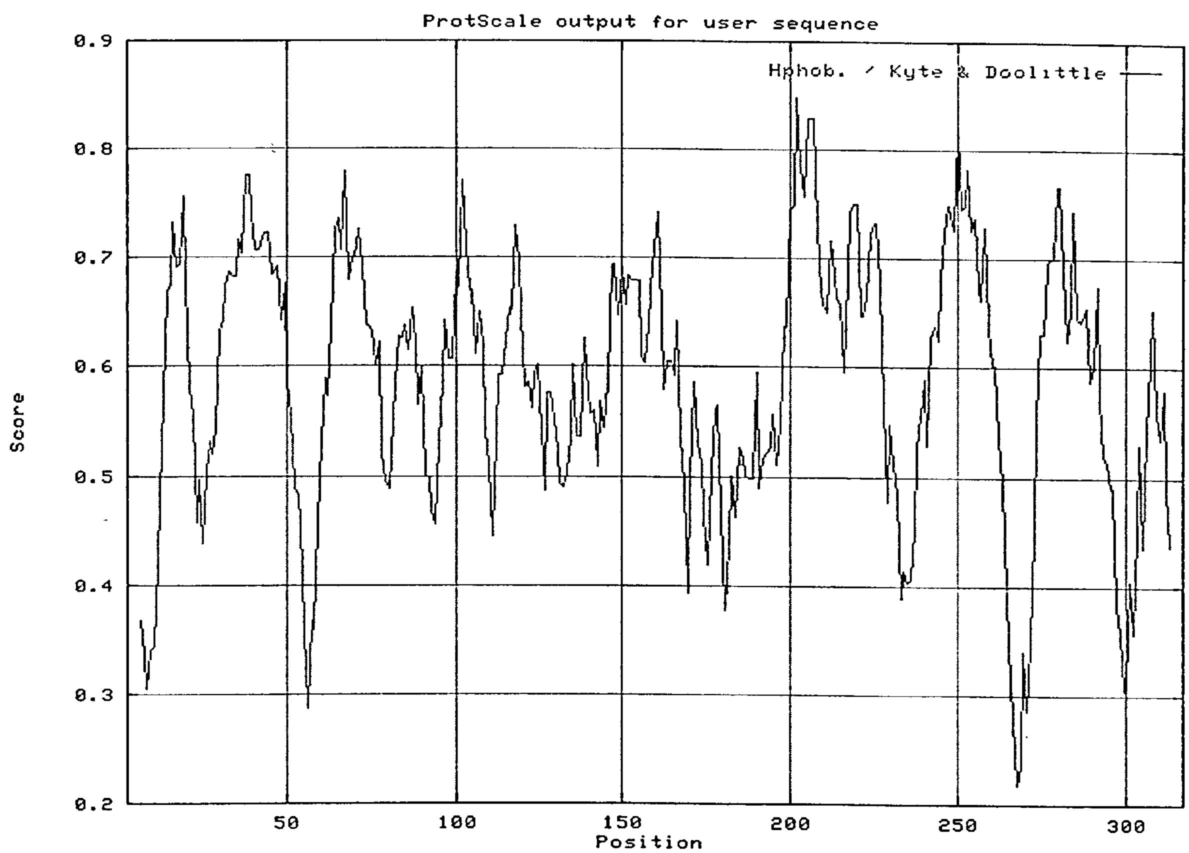


Figure 7:
101P3A11 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

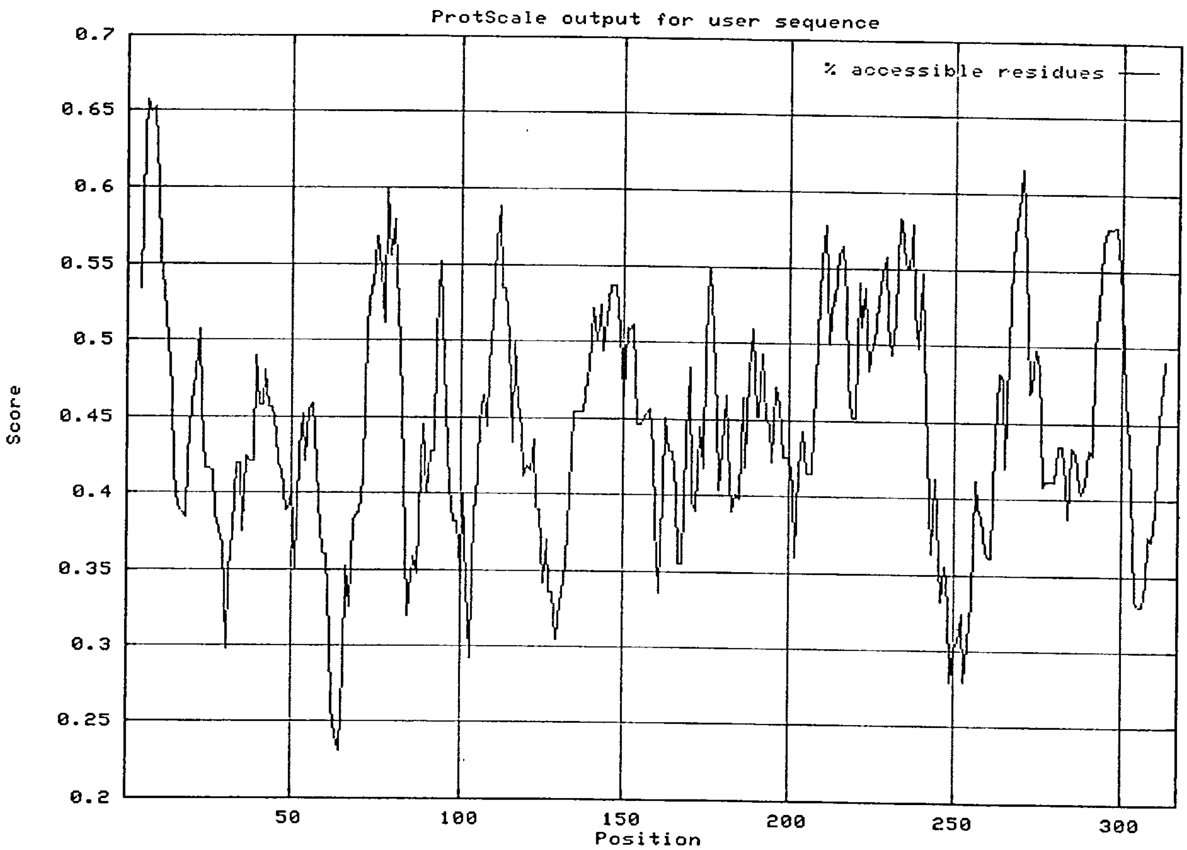


Figure 8:
101P3A11 Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

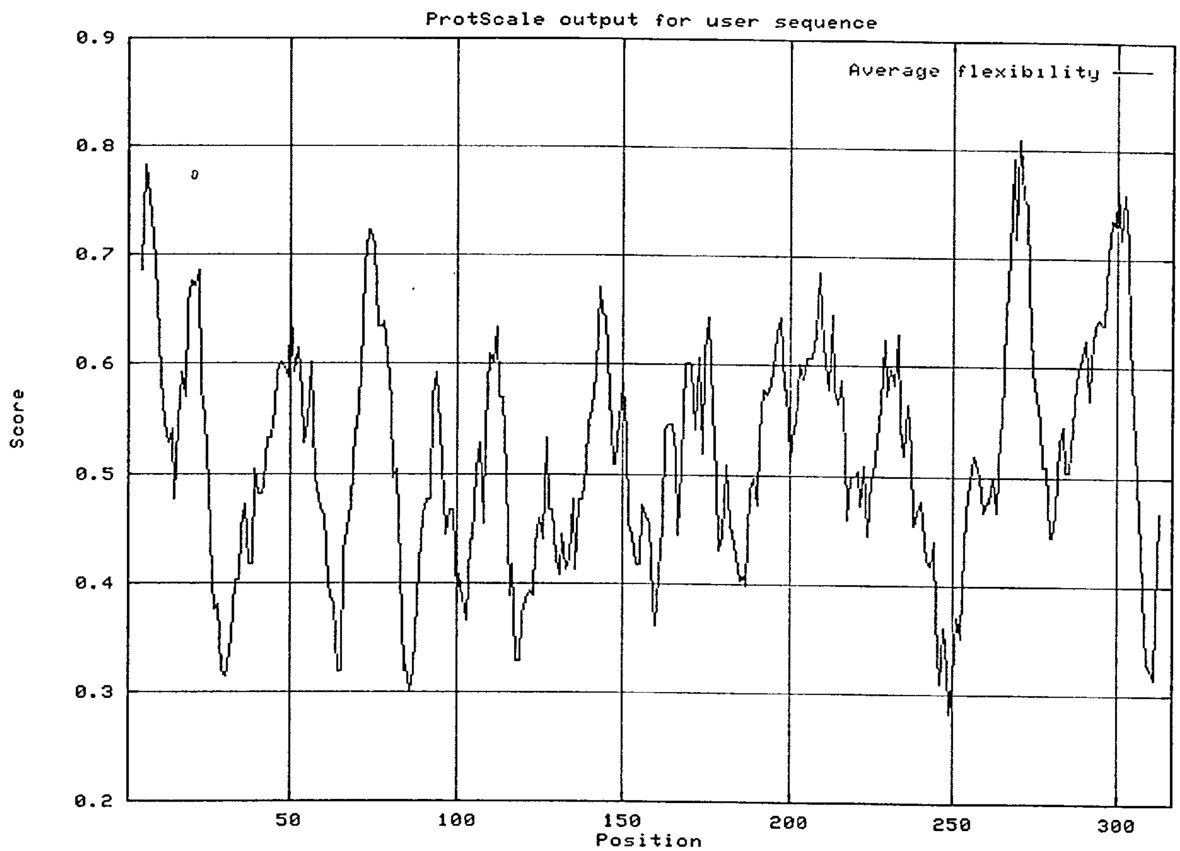
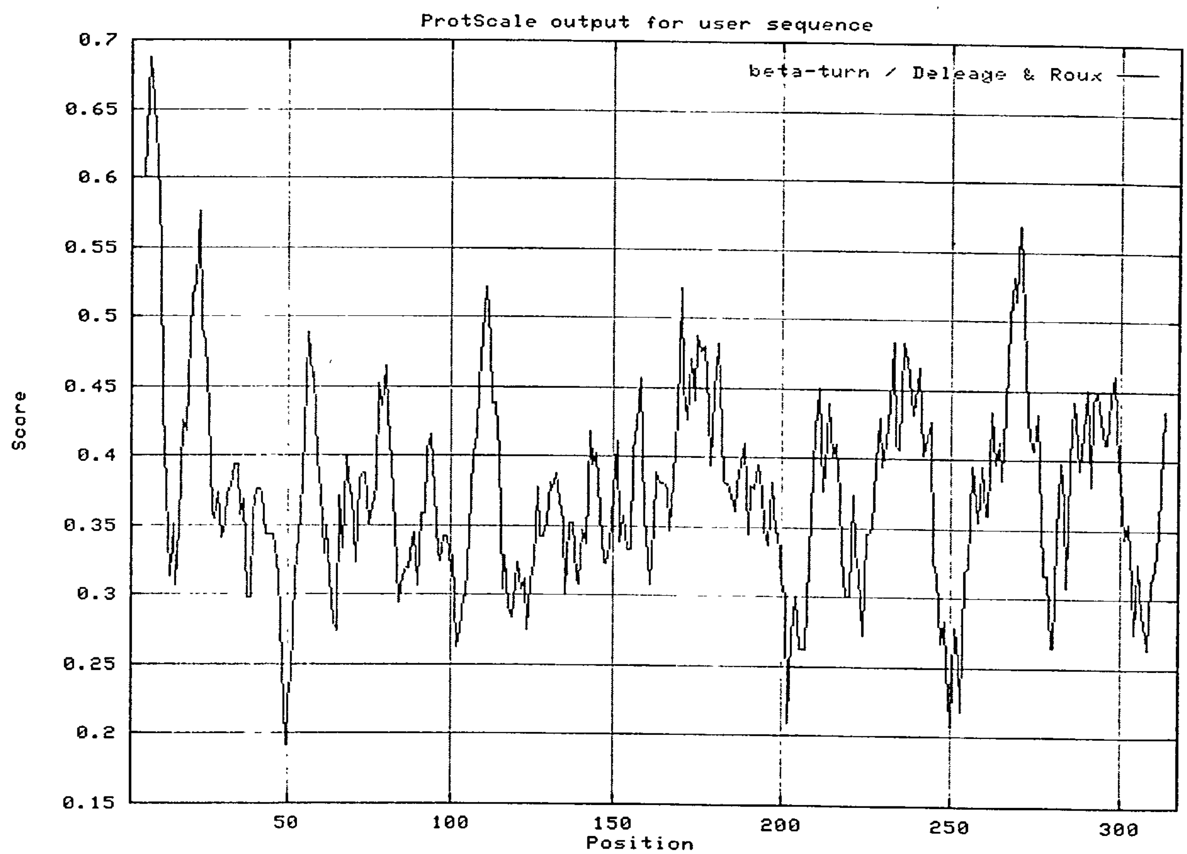


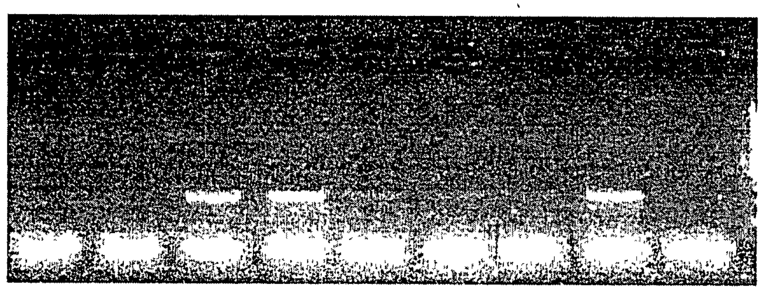
Figure 9:
101P3A11 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)



[redacted]

Figure 10A. Expression of 101P3A11 by RT-PCR

1 2 3 4 5 6 7 8 9



- VP1 (Kidney, Lung, Liver)
- VP2 (Pancreas, Colon, Stomach)
- Prostate xenograft Pool
- Prostate Cancer Pool
- Kidney Cancer Pool
- Colon Cancer Pool
- Breast Cancer Pool
- Metastasis Pool
- H2O

Figure 10B

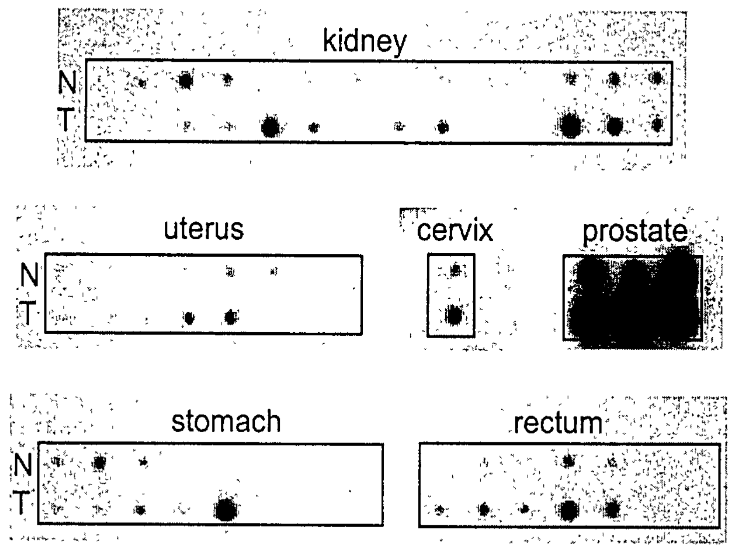
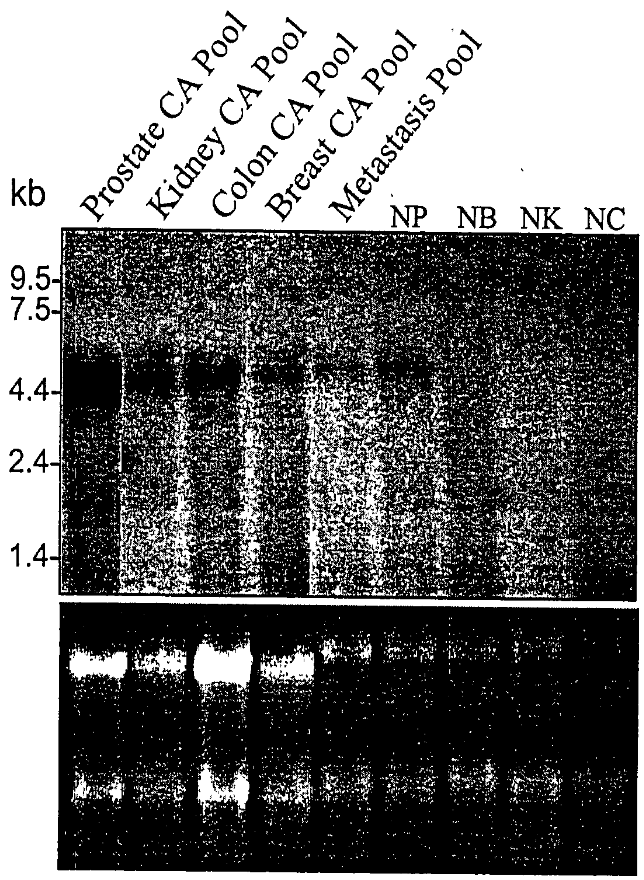


Figure 11. **Expression of 101P3A11 in Human Patient Cancer Specimens**

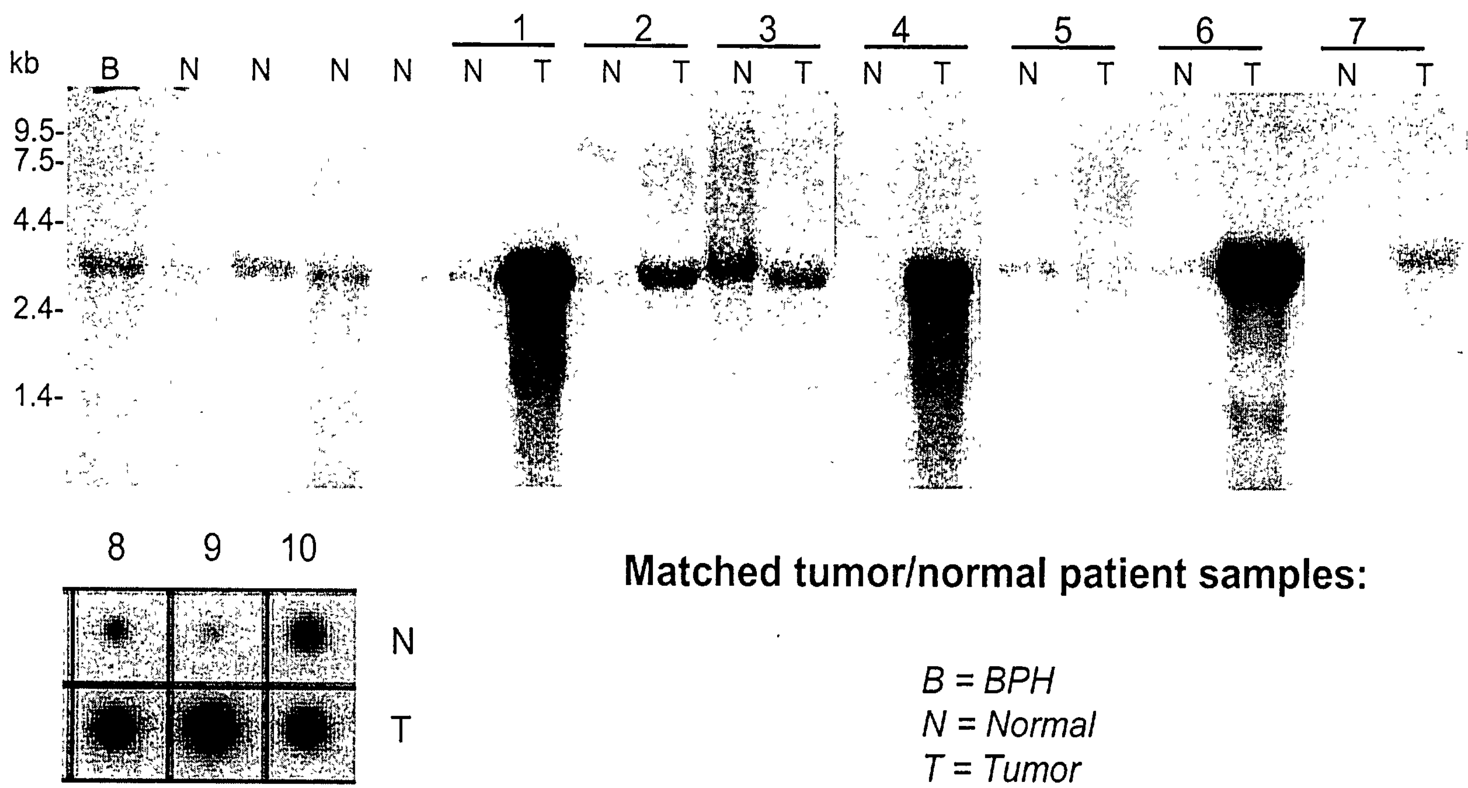


10µg total RNA/per lane from a pool of 3 tumors as follows:

Prostate Cancer Pool = gleason 6, 8, 9
Kidney Cancer Pool = grade 2, 2, 3
Colon Cancer Pool = stage II, III, IV
Breast Cancer Pool = grade 1, 2, 3
Metastasis Pool = colon to lung, colon to liver, ovary to fall. tube

NP = Normal Prostate
NB = Normal Bladder
NK = Normal Kidney
NC = Normal Colon

Figure 12A



Matched tumor/normal patient samples:

B = BPH
N = Normal
T = Tumor

Figure 12B and 12C

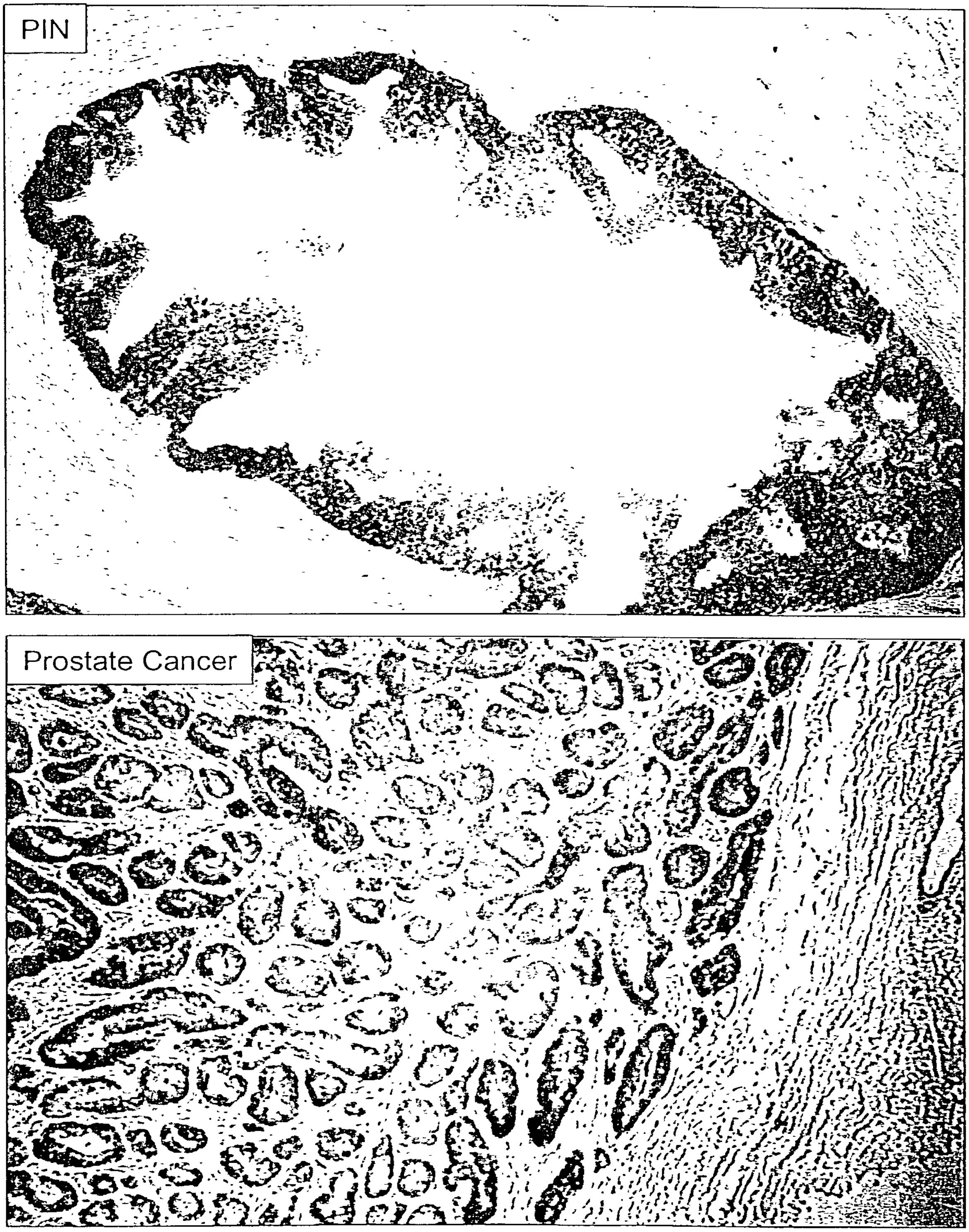


Figure 12D and 12E

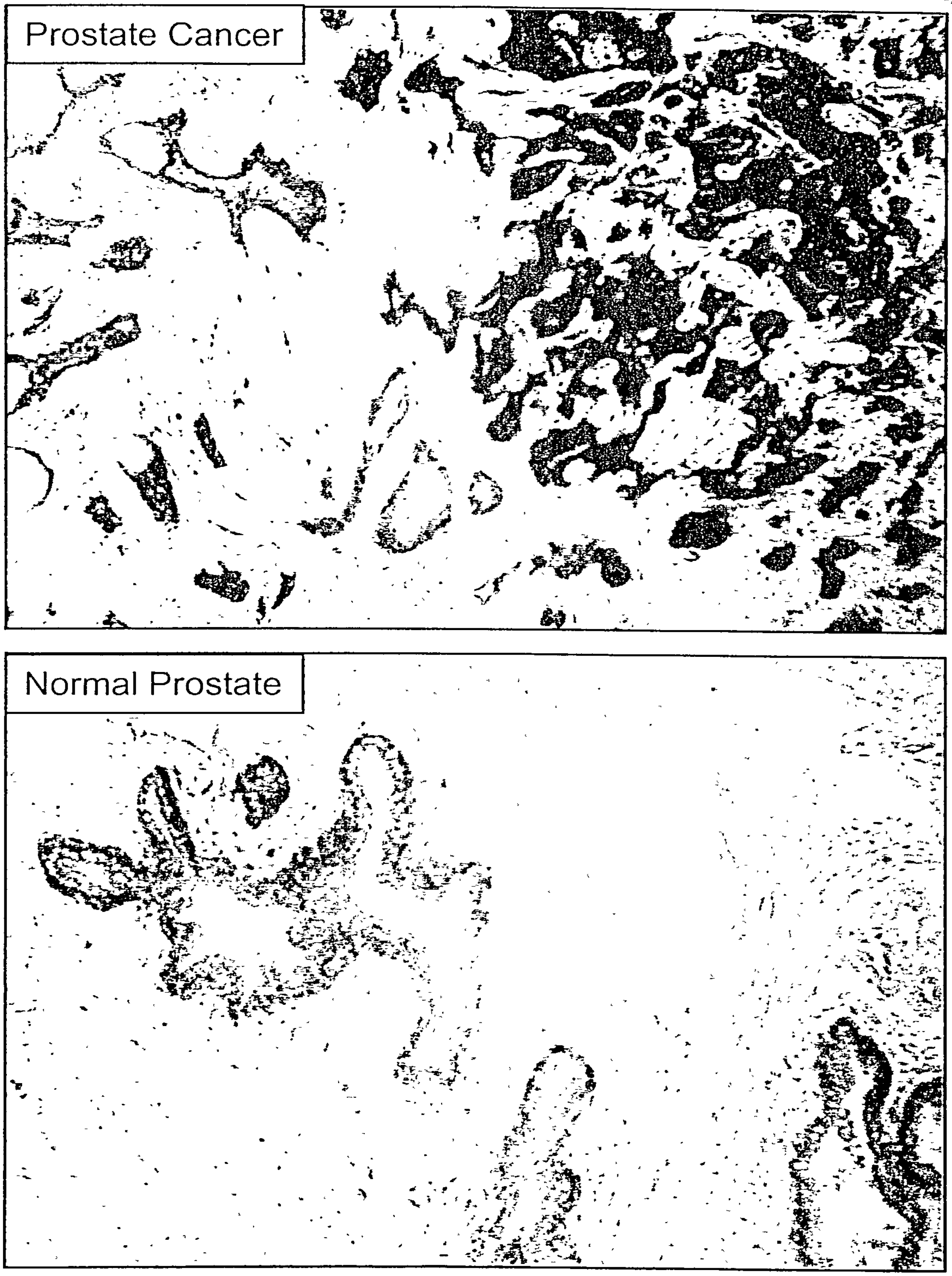
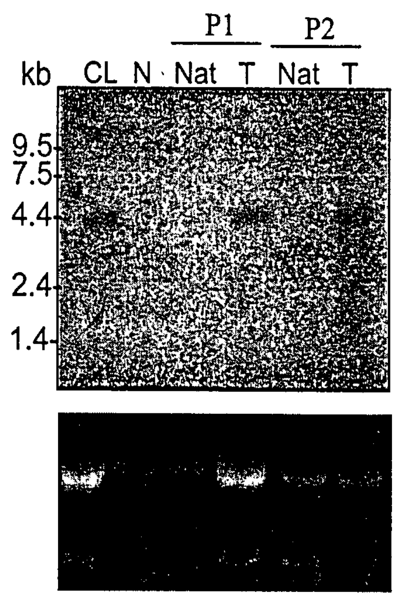


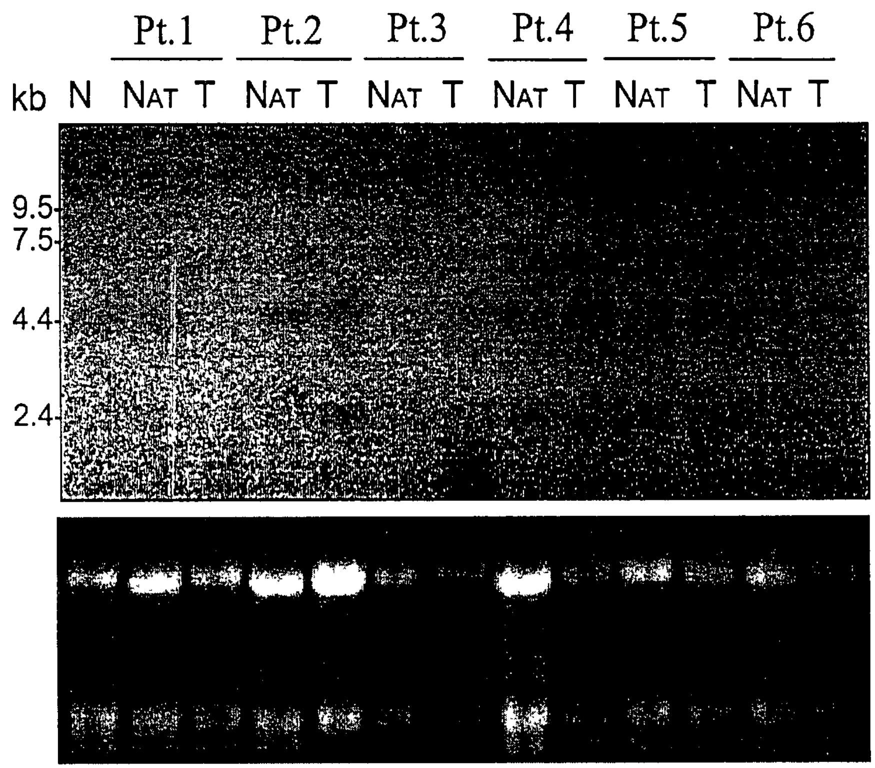
Figure 13. Expression of 101P3A11 in Colon Cancer Patient Specimens



P1, Stage I
P2, Stage IV

CL = *Colon cancer cell line T84*
N = *Normal colon*
Nat = *Normal Adjacent Tissue*
T = *Tumor*

Figure 14. Expression of 101P3A11 in Kidney Cancer Patient Specimens



Pt.1, Papillary carcinoma, stage I
Pt.2, Invasive papillary carcinoma
Pt.3, Clear cell type grade 1/3, focally 2/3
Pt.4, Clear cell type, stage III
Pt.5, Clear cell type, stage III
Pt.6, Clear cell type, stage III

N = Normal kidney
NAT = Normal adjacent tumor
T = Tumor

Figure 15A-15C. Androgen Regulation of 101P3A11 in Tissue Culture Cells

- LAPC-9 cell line charcoal-stripped FBS, 14 hrs
- LAPC-9 cell line charcoal-stripped FBS, 14 hrs + mibolerone
- LAPC-9 cell line charcoal-stripped FBS, 24 hrs
- LAPC-9 cell line charcoal-stripped FBS, 24 hrs + mibolerone

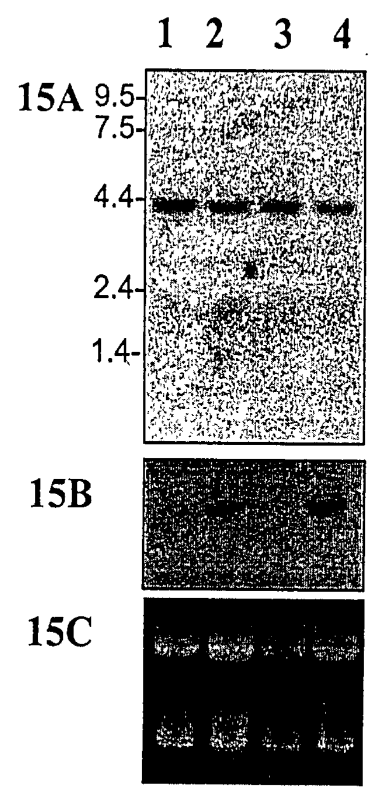
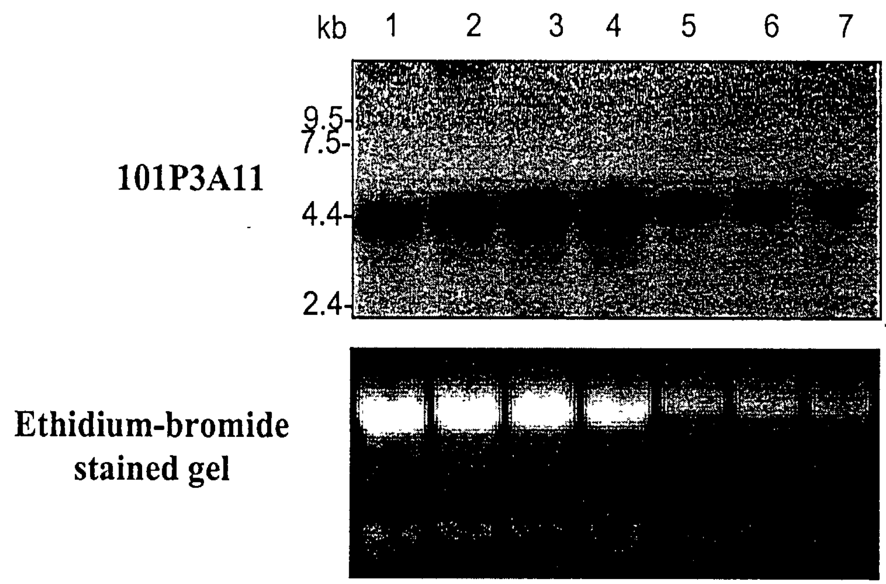


Figure 16. Androgen Regulation of 101P3A11 *In Vivo*



- LAPC-9AD Day 0 Mouse #1
- LAPC-9AD Day 0 Mouse #2
- LAPC-9AD Day 7 Mouse #3
- LAPC-9AD Day 7 Mouse #4
- LAPC-9AD Day 15 Mouse #5
- LAPC-9AD Day 15 Mouse #6
- LAPC-9AD Day 21 Mouse #7

Figure 17. Expression and Detection of 101P3A11(159-202)-psecFc Fusion Protein

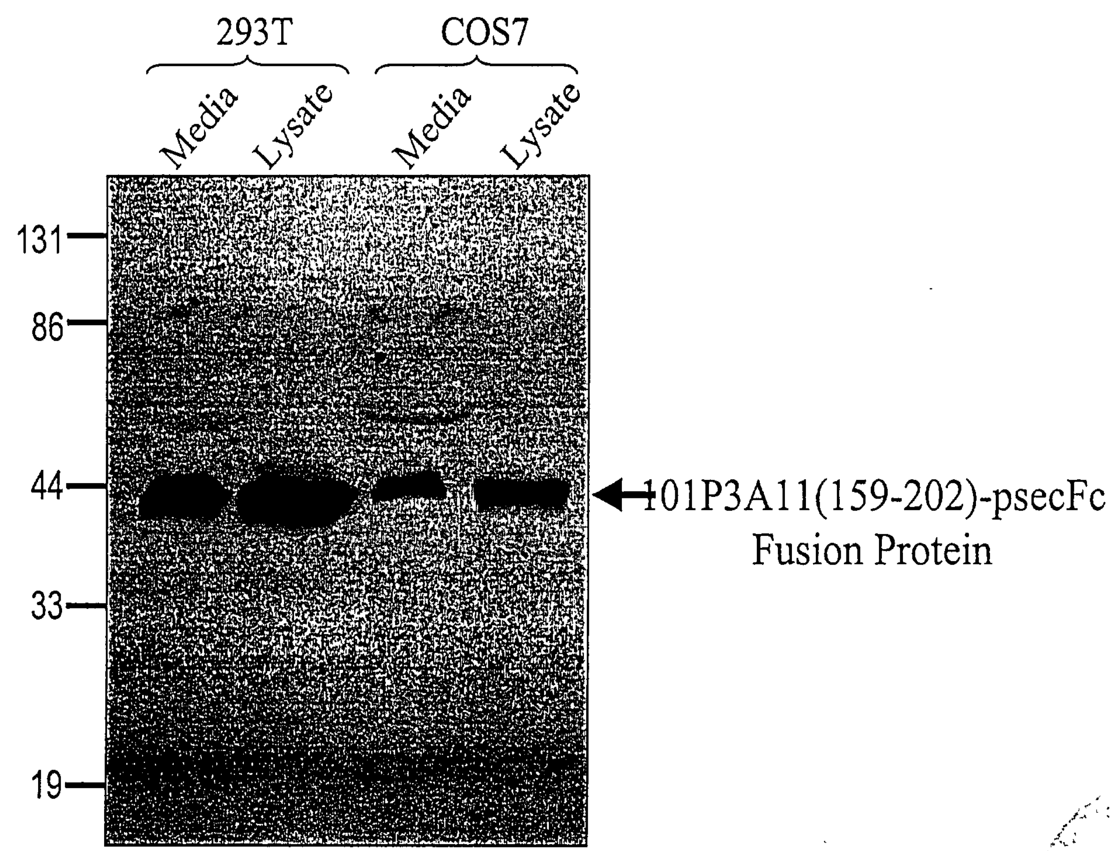
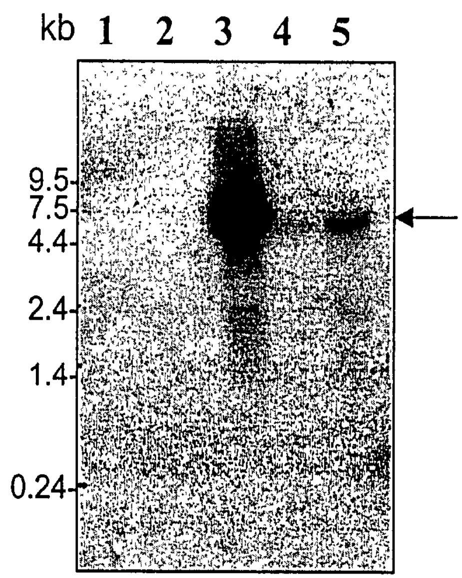


Figure 18. Expression of 101P3A11 in 300.19 Cells



- 300.19
- 300.19/neo-pSRα
- 300.19/101P3A11-pSRα
- LAPC-4AD
- LAPC-9AD

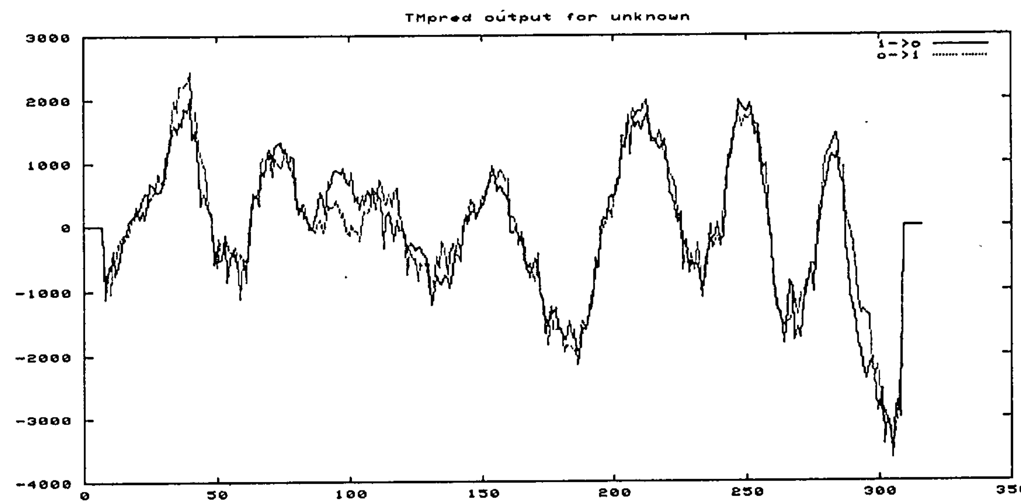
Figure 19A. Secondary structure prediction of 101P3A11

```
        10        20        30        40        50        60        70
         |         |         |         |         |         |         |
MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSG
cccccccccceeeeeeeecccchhhhhhhhhcchhhhhhhhhcccceeeeeeeeccccchhhhhhhhhhcc
IDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTL
ceeeeecccchhhhheeeecccccceehhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhcccccceeeeec
PRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIG
cccheehhhhhhhhhhhcchhhhecccccccchhcchhhhhhhhhhhhhhceeeeeeeeeeeeehhc
LDSLLISFSYLLILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANI
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccceeeeeeeeeeeehchcchhhhhhcccccccccheeeeeh
YLLVPPVLNPIVYGVKTKEIRQRILRLFHVATHASEP
hhhcccccccheeeecchhhhhhhhhhhhheeeccccccc
```

c: random coil (30.60%)
e: extended strand (21.45%)
h: alpha helix (47.95%)

Figure 19B-19C. Transmembrane prediction of 101P3A11

19B



19C

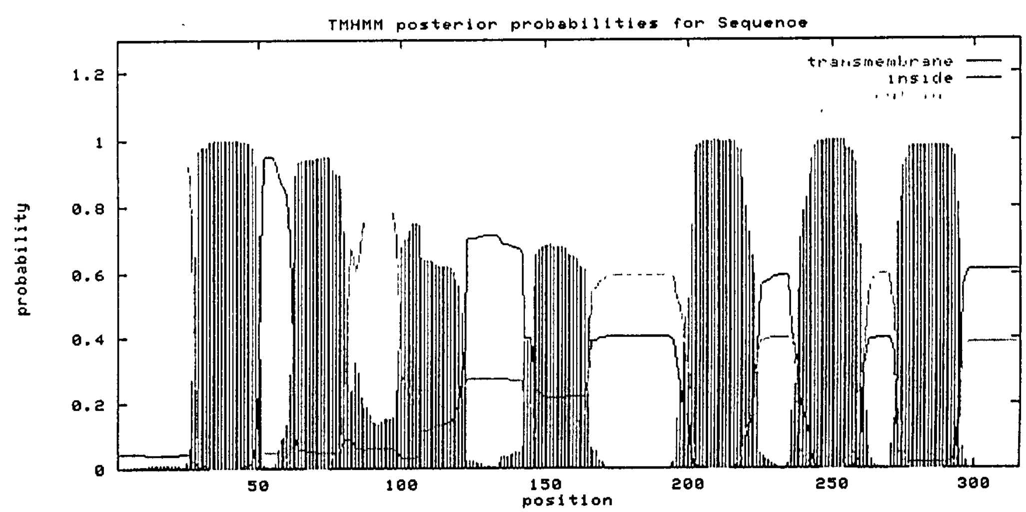


Figure 20. Expression of 101P3A11 in NIH-3T3 Tumors

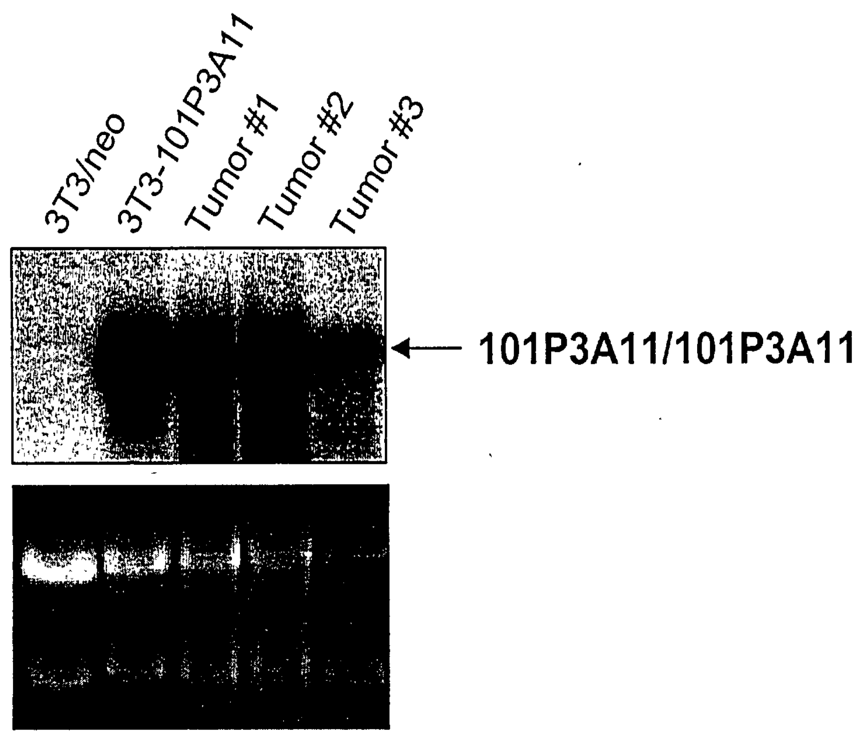
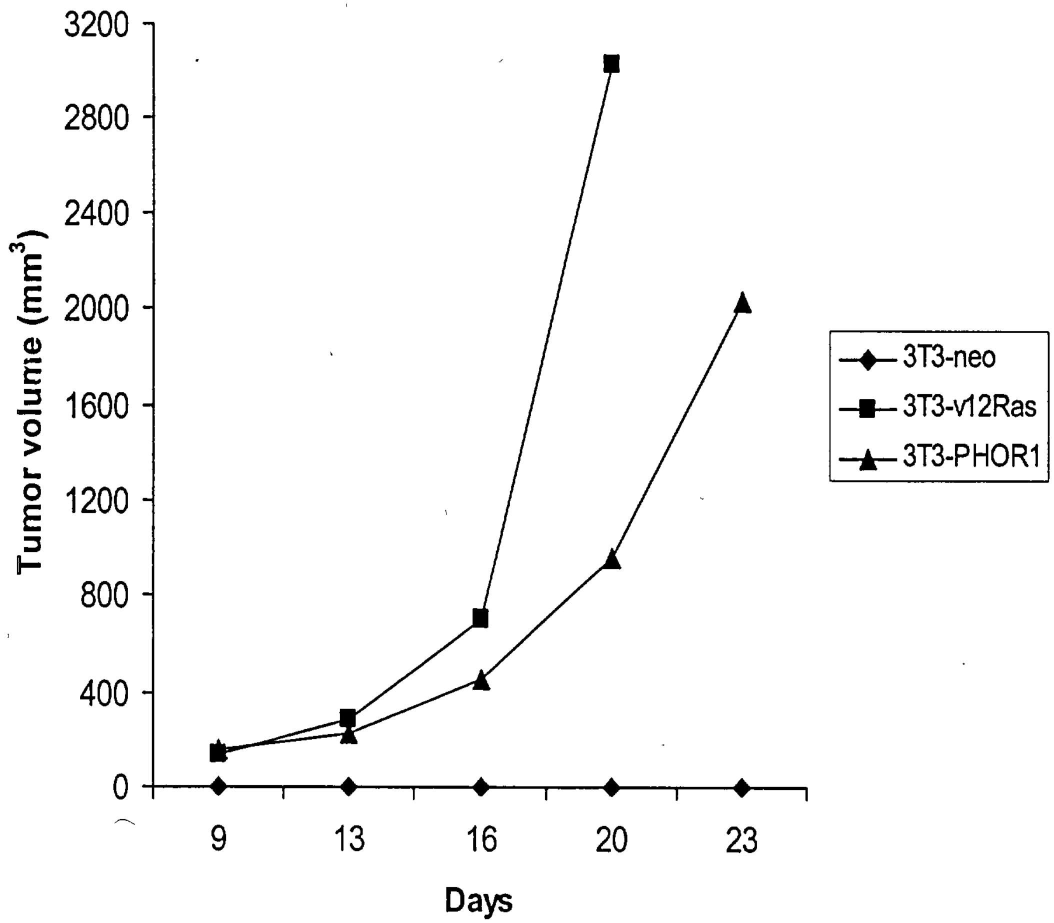
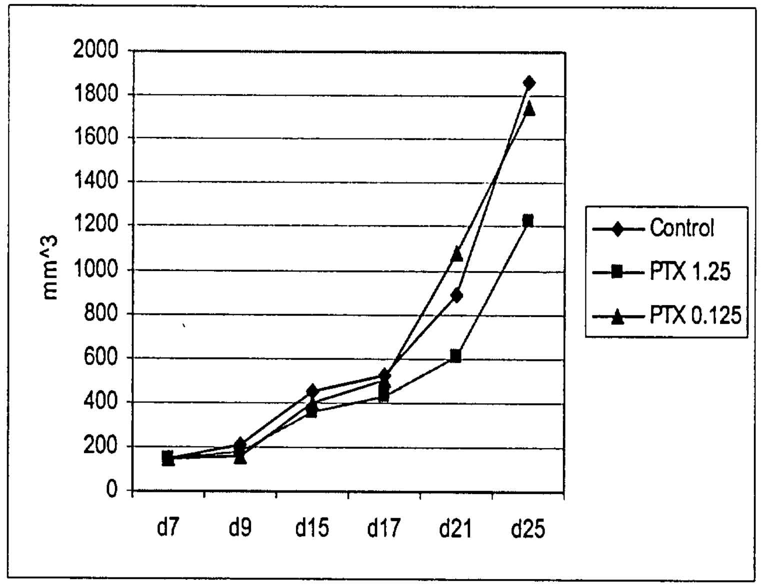


Figure 21: 101P3A11 Induces Tumor Formation of 3T3 Cells



•Injection of 10^6 3T3-neo, 3T3-Ras or 3T3-101P3A11 cells subcutaneously into SCID mice revealed that 6/6 3T3-Ras-injected mice formed tumors, 6/6 3T3-101P3A11- injected mice formed tumors, and 0/6 3T3-neo-injected mice formed tumors.

Figure 22: PTX Reduces the *in vivo* Growth of 3T3-101P3A11 Tumors



•Pertussis toxin inhibits the sub-cutaneous growth of 3T3-101P3A11 tumors in SCID mice.

•The inhibitory activity of pertussis toxin occurs in a dose dependent manner.

Figure 23: Alignment of 101P3A11-PHOR-1 with the rat GPCR RA1C (gi|3420759).

Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%)

```
PHOR: 14  FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
          F+LIG+PGLEEA FW  FPL S+Y +A+ GN  +++IVRTE SLH PMY+FLCML+ ID+
RA1C: 11  FMLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70

PHOR: 74  LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
           +STS+MPK+LA+FWF+S  I FDACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
RA1C: 71  ALSTSTMPKILALFWFDSREITFDACLAQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
          HA VL      +IG+ A+VRG+    PLP+ IK+L FC SN+LSHSYC+HQDVMKLA  D
RA1C: 131 HAAVLNNTVTVQIGMVALVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYTD 190

PHOR: 194 IRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
             NVVYGL  I+  +G+D + IS SY LI++ VL L ++   +AKAFGTCVSH+  V  F
RA1C: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSHIGVVLAF 250

PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311
          YVP IGLS+VHRF    D  + V++ ++YLL+PPV+NPI+YG KTK+IR R+L +F ++
RA1C: 251 YVPLIGLSVVHRFGNSLDPIVHVLMGDVYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309
```

Figure 24: Alignment of 101P3A11-PHOR-1 with the human prostate specific GPCR.(gi|13540539)

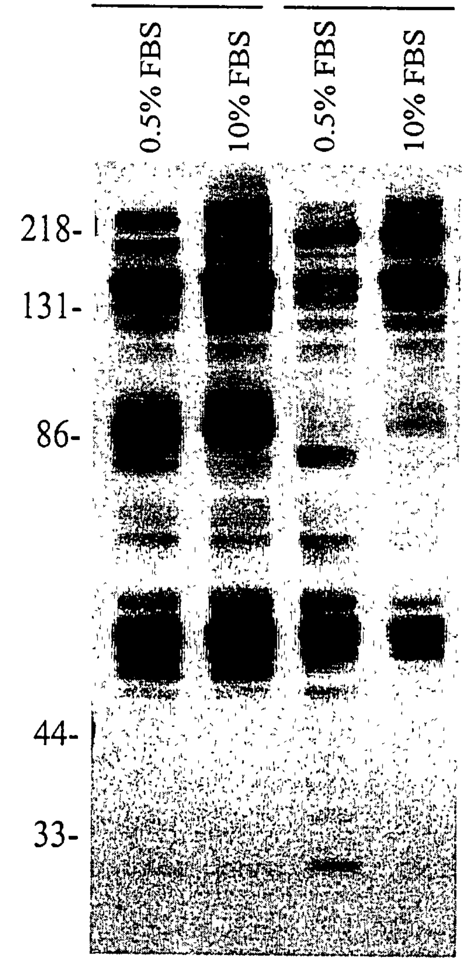
Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%)

```
PHOR: 14   FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
           F+LIG+PGLE+A FW+ FPL S+Y++A+ GN  +++IVRTE SLH PMY+FLCML+ ID+
GPCR: 11   FVLIGIPGLEKAHFWVGFPLLSMYVVAMFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70

PHOR: 74   LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
            +STS+MPK+LA+FWF+S  I F+ACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
GPCR: 71   ALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134  HATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
           HA VL      +IG+ AVVRG+    PLP+ IK+L FC SN+LSHSYC+HQDVMKLA  D
GPCR: 131  HAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYAD 190

PHOR: 194  IRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
              NVVYGL  I+  +G+D + IS SY LI++TVL L ++  +AKAFGTCVSH+  V  F
GPCR: 191  TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAF 250

PHOR: 253  YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311
           YVP IGLS+VHRF       + V++ +IYLL+PPV+NPI+YG KTK+IR R+L +F ++
GPCR: 251  YVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309
```

Figure 25: Alignment with human olfactory receptor 5I12 (gi|14423836)

```
Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%)

PHOR: 7   NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLC 66
          N +   +F+L G+PGLE +  WL+ PLC +Y +A+ GN  I+  VR E SLHEPMY FL
HOR5: 5   NVTHPAFFLLTGIPGLESSHSWLSGPLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFLS 64

PHOR: 67  MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126
          MLS  D+ IS +++P +L  F  N+  I FDACL+Q+F IH  S MES +LLAM+FDRYV
HOR5: 65  MLSFSDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYV 124

PHOR: 127 AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186
          AIC PLR+ATVLT   +  +G+ A  R    + PLP  IK+LP CRSN+LSHSYCLH D+
HOR5: 125 AICDPLRYATVLTTEVIAAMGLGAAARSFITLFPLPFLIKRLPICRSNVLSHSYCLHPDM 184

PHOR: 187 MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245
          M+LAC DI +N +YGL V++S  G+D   I  SY+LIL++V+   +RE + KA  TCVSH
HOR5: 185 MRLACADISINSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSH 244

PHOR: 246 VCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRIL 305
          + AV  FYVP IG+S VHRF K     + V+++N+YL VPPVLNP++Y  KTKEIR+ I
HOR5: 245 ILAVLAFYVPMIGVSTVHRFGKHVPCYIHVLMSNVYLFVPPVLNPLIYSAKTKEIRRAIF 304

PHOR: 306 RLFH 309
          R+FH
HOR5: 305 RMFH 308
```

Figure 26: 101P3A11 Modulated Tyrosine Phosphorylation in NIH-3T3 Cells



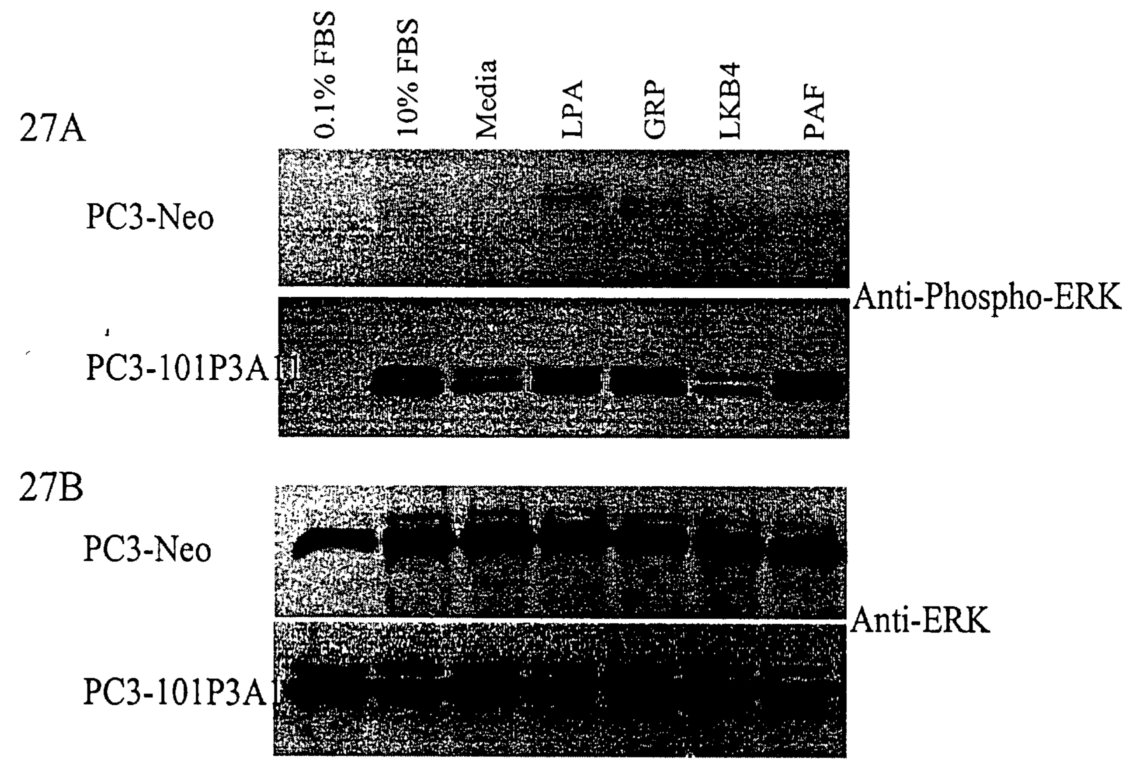
Anti-PY Blot

•101P3A11 mediated the de-phosphorylation of proteins at 200, 120-140, 85-90 and 55 kDa

•101P3A11 induced the phsophorylation of proteins at 80 and 29 kDa in NIH-3T3 cells.

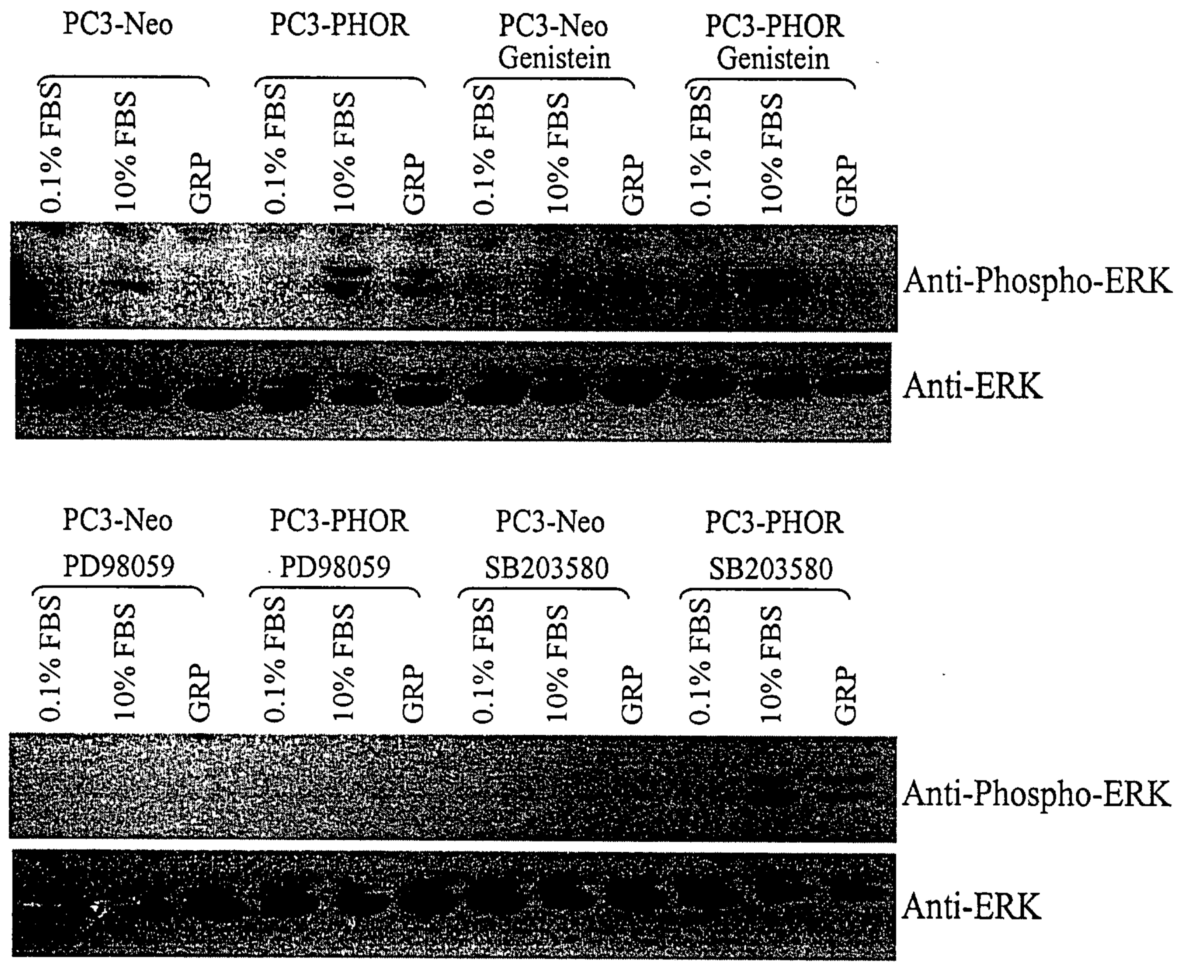
3

Figures 27A-27B: ERK Phosphorylation by PCR Ligands in 101P3A11 Expressing Cells



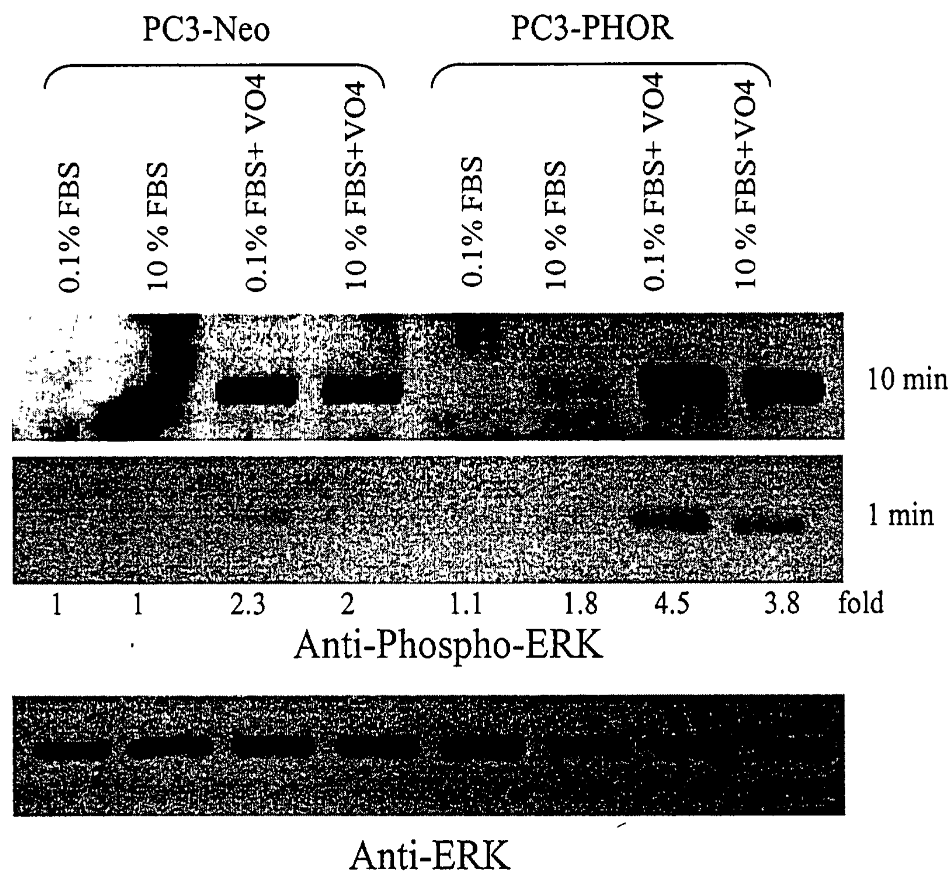
•FBS, lipophosphatidic acid, gastrin releasing peptide, leukotriene and platelet activating factor induced the phosphorylation of ERK in 101P3A11 expressing cells.

Figure 28: Inhibition of 101P3A11-Mediated ERK Activation by PD98059



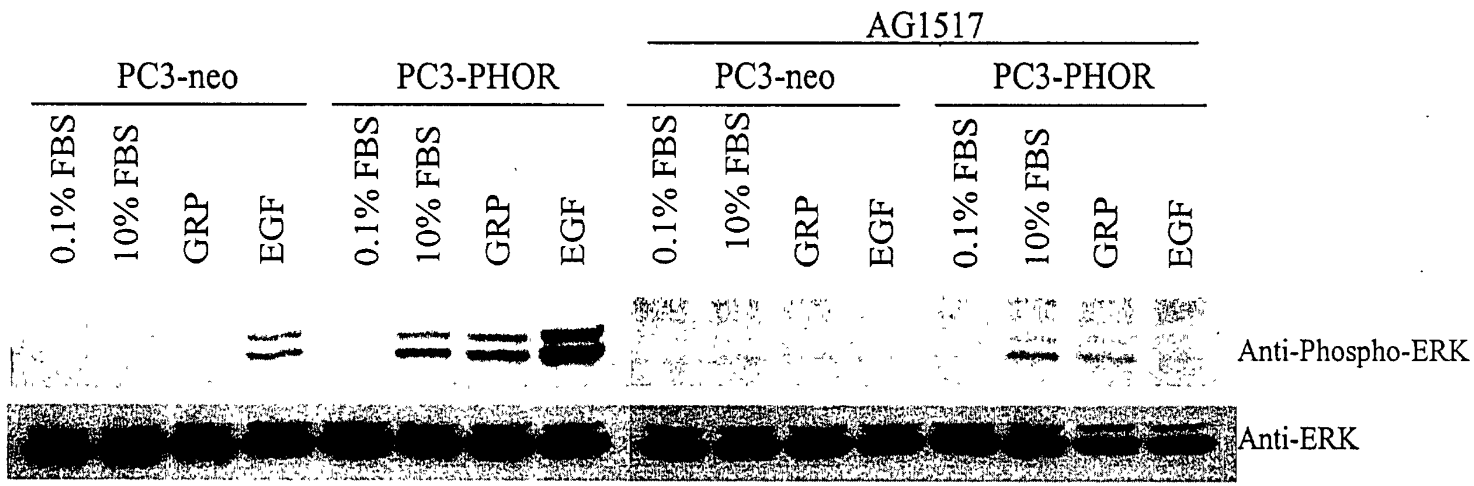
•ERK phosphorylation was inhibited by a MEK specific(PD98059) but not a p38 specific (SB203580) inhibitor in PC3-101P3A11 cells.

Figure 29: Enhanced ERK Phosphorylation in Sodium Orthovanadate Treated PC3-101P3A11 Cells



•Sodium orthovanadate induced increased ERK phosphorylation in PC3-101P3A11 cells relative to PC3-neo cells.

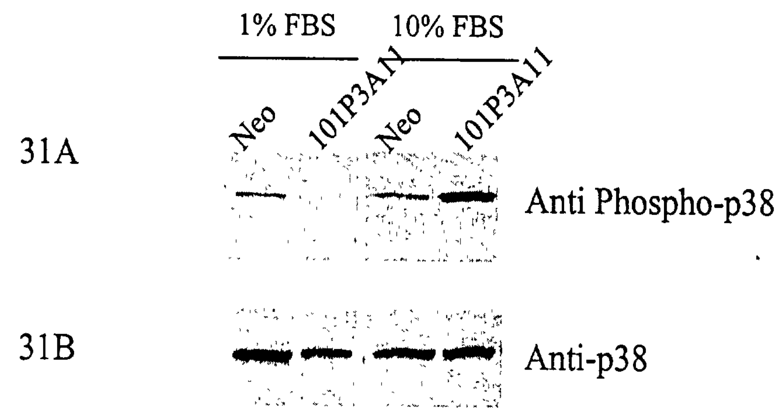
Figure 30: Inhibition of 101P3A11-Mediated ERK Phosphorylation by AG1517



•The EGFR inhibitor, AG1517, inhibits EGF-mediated ERK phosphorylation in control and 101P3A11 expressing PC3 cells.

•AG1517 partially inhibits 101P3A11 mediated ERK phosphorylation in PC3 cells.

Figure 31A-31B: Activation of p38 in PC3-101P3A11 Cells



•Expression of 101P3A11 mediates p38 phosphorylation in cells treated with 10% FBS.

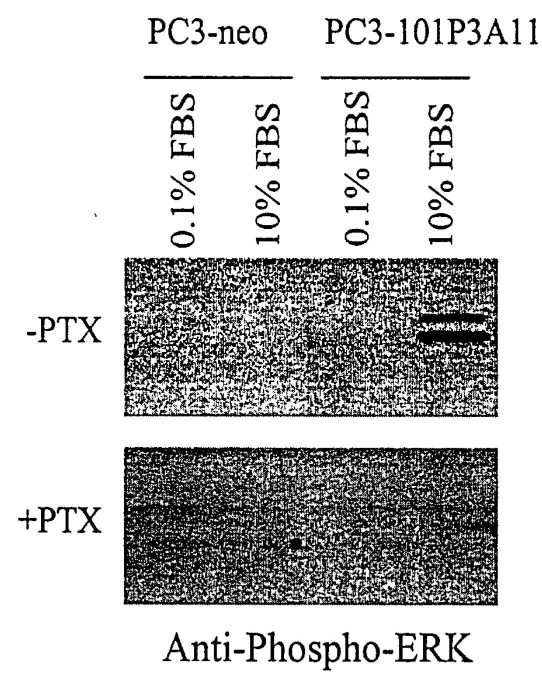
Figure 32: 101P3A11 Induced Accumulation of cAMP in PC3 Cells

		Fold change in [cAMP]	
		PC3-Neo	PC3-PHOR
0.1%FBS	-PTX	1	4.302
	+PTX	1.403	2.577
10%FBS	-PTX	2.738	6.978
	+PTX	2.163	2.752

Fold Change in cAMP accumulation was calculated relative to PC3-neo cells grown in 0.1%FBS

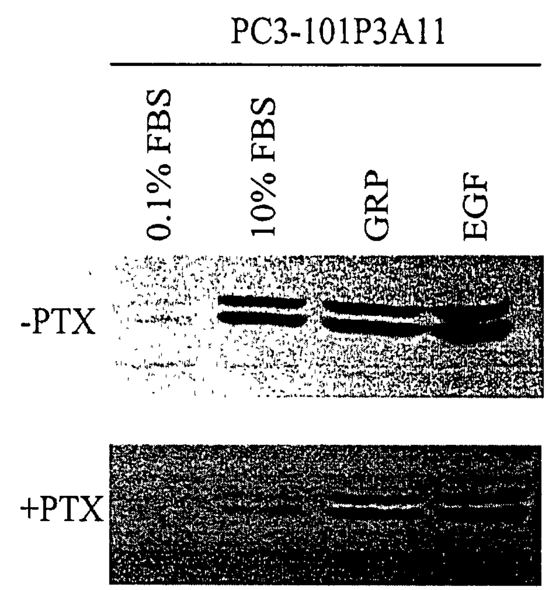
- Expression of 101P3A11 increased the accumulation of cAMP in cells treated with 0.1% and 10% FBS.
- FBS-induced cAMP accumulation in 101P3A11 cells was inhibited by pertussis toxin.

Figure 33: Pertussis Toxin Inhibits 101P3A11 Mediated ERK Phosphorylation



•Pertussis toxin inhibited FBS- mediated ERK phosphorylation in 101P3A11 expressing cells.

Figure 34: Pertussis Toxin Inhibited ERK Phosphorylation in PC3-101P3A11 Cells

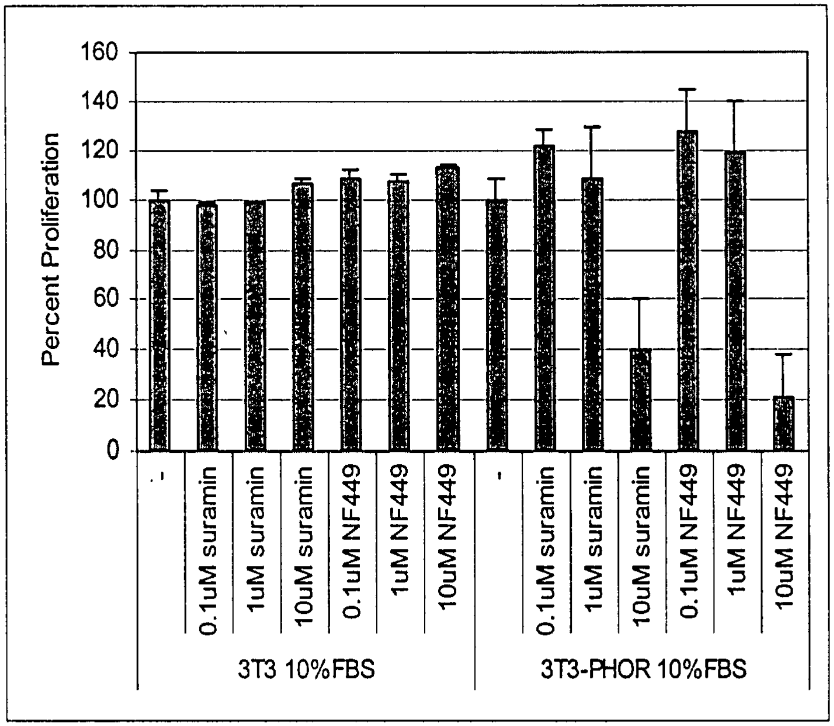


Anti-Phospho-ERK

•Pertussis toxin inhibited FBS- mediated ERK phosphorylation in 101P3A11 expressing cells.

•The inhibitory activity of pertussis toxin on ERK phosphorylation was more dramatic in FBS-treated than EGF or GRP-treated PC3-101P3A11 cells.

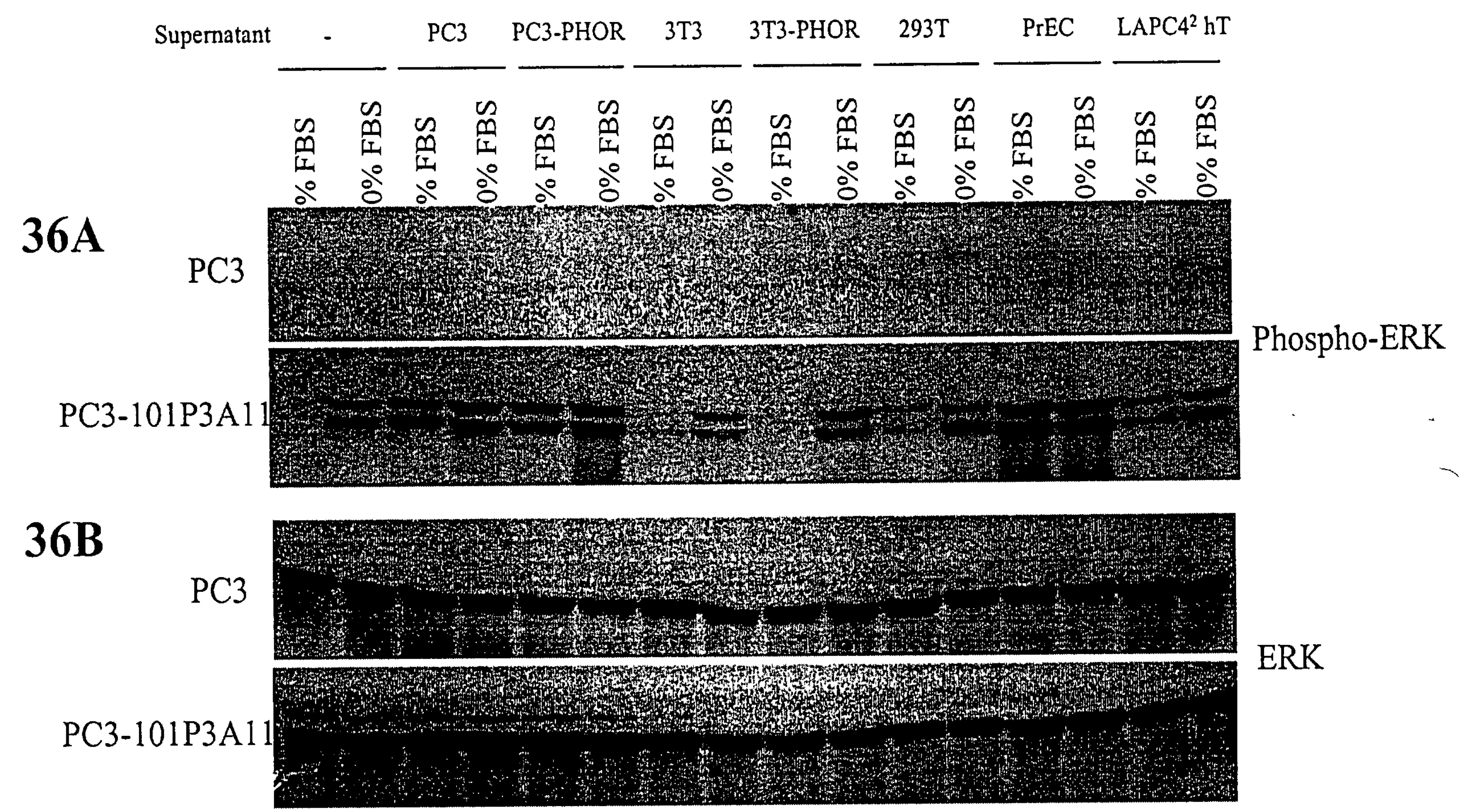
Figure 35: Inhibition of 101P3A11 Mediated Signaling by Suranim



•Control NIH 3T3 and 3T3-101P3A11 cells were grown in the presence of absence of G protein inhibitors suranim and NF449. Proliferation was analyzed by Alamar blue after 72 hours.

•Suranim and NF449 inhibited the proliferation of 101P3A11 expressing but not control cells.

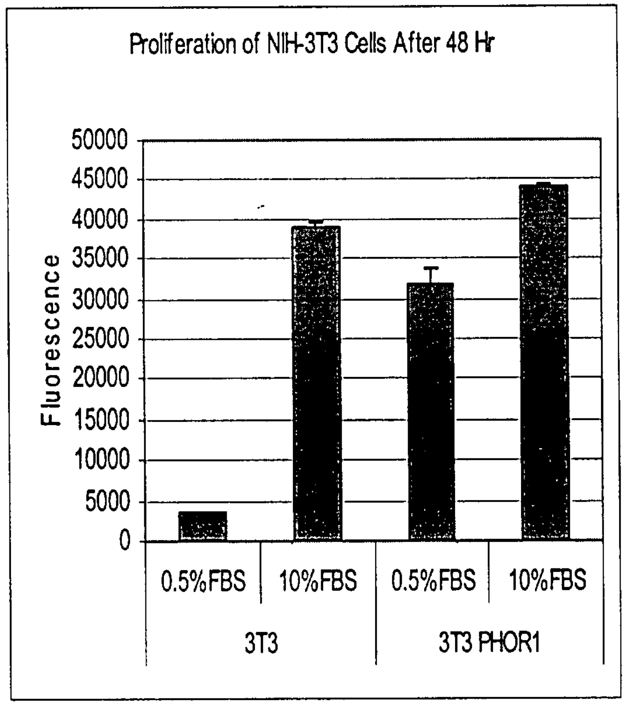
Figures 36A-36B: 101P3A11 Mediated ERK Phosphorylation By Conditioned Media



•Supernatants from PC3, PC3-101P3A11, PrEC and LAPC4[2] cells induce ERK phosphorylation in PC3 101P3A11 but not PC3 cells.

•Supernantants from 3T3 and 293T cells had little specific effect on ERK phosphorylation.

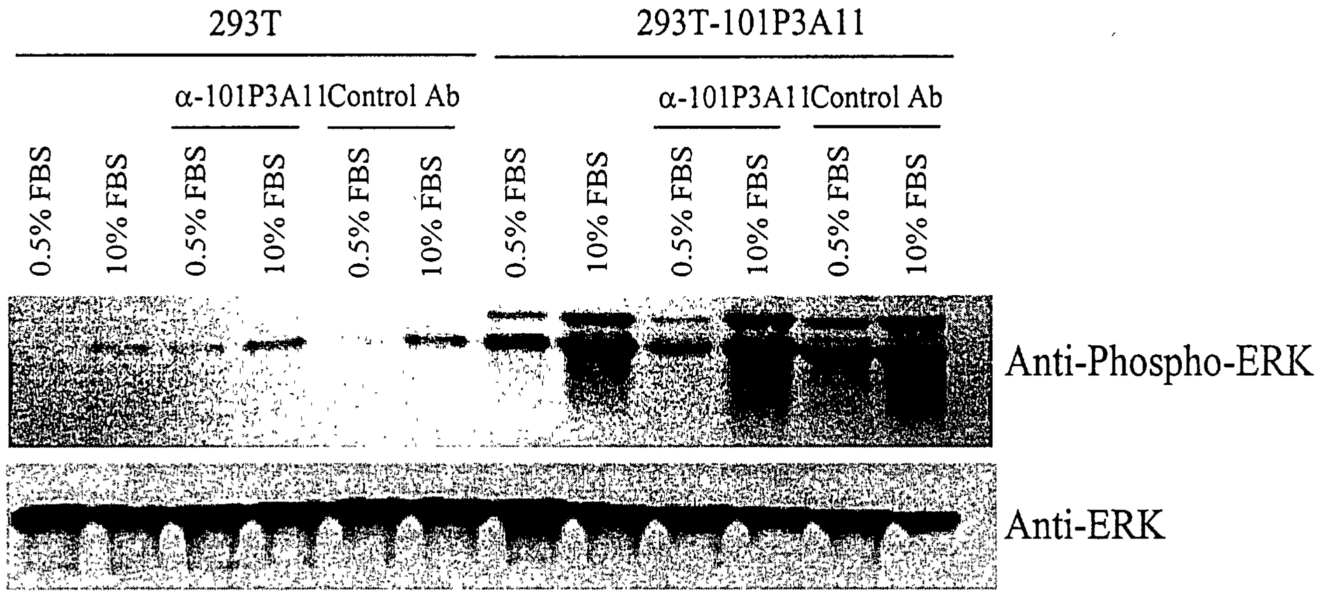
Figure 37: 101P3A11 Enhances The Proliferation of 3T3 Cells



•Control NIH 3T3 and 3T3-101P3A11 cells were grown in the presence of absence 0.5 or 10% FBS. Proliferation was analyzed by Alamar blue after 48 hours.

•Expression of 101P3A11 induced a 6 fold increase in the proliferation of 3T3 cells grown in 0.5% FBS.

Figure 38: Inhibition of 101P3A11 Mediated ERK Phosphorylation by 101P3A11 Specific Antibodies

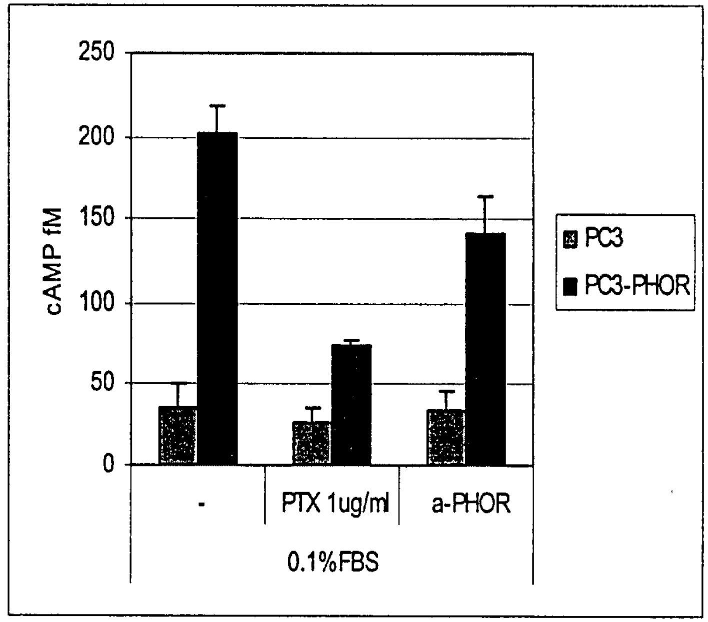


•Expression of 101P3A11 induced ERK phosphorylation in 293T cells.

•Anti-101P3A11 pAb inhibited ERK Phosphorylation in 293T-101P3A11 cells .

Figure 39: Anti-101P3A11 Ab Mediated cAMP Accumulation in PC3-101P3A11 Cells

	Fold Increase in cAMP	
Treatment	PC3	PC3-PHOR
0.1% FBS	1± 0.42	5.73 ± 0.47
PTX 1ug/ml	0.74± 0.28	2.12 ± 0.09
anti-PHOR	0.97± 0.35	4.01± 0.64



•Control PC3 cells and cells expressing 101P3A11 were treated with anti-101P3A11 pAb for 2 min and evaluated for intracellular cAMP content.

•The assay was performed in duplicate.

Figure 40A-40F

Fig. 40A. Prostate Cancer, 400X

Fig. 40D. LNCaP, 400X

Fig. 40B. Prostate Cancer, 400X

Fig. 40E. Prostate, 400X

Fig. 40C. Prostate Cancer, 2000X

Fig. 40F. Prostate, 2000X

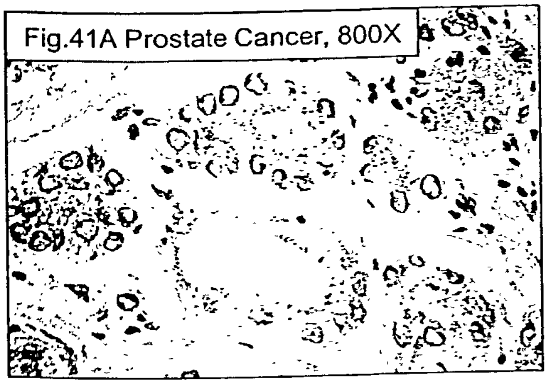


Fig.41A Prostate Cancer, 800X

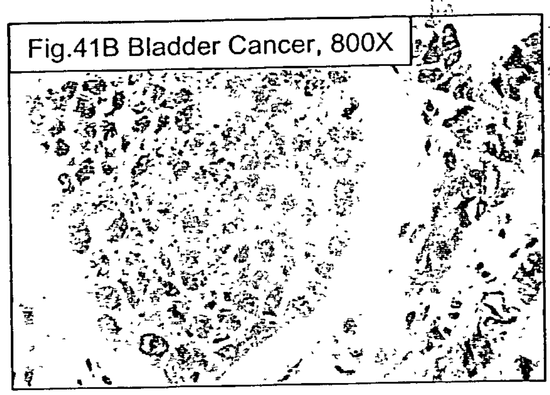


Fig.41B Bladder Cancer, 800X

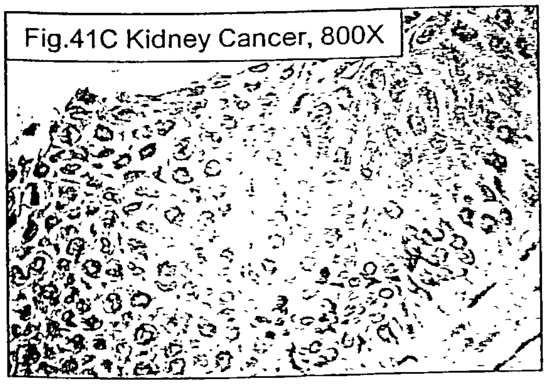


Fig.41C Kidney Cancer, 800X

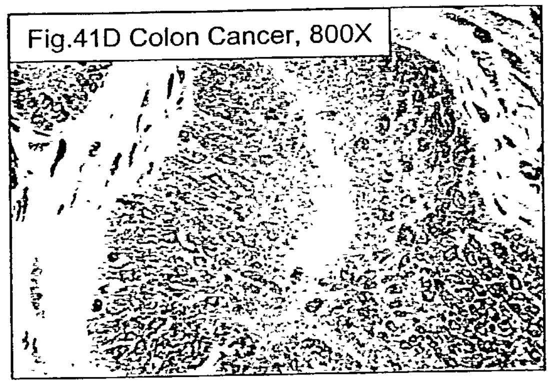


Fig.41D Colon Cancer, 800X

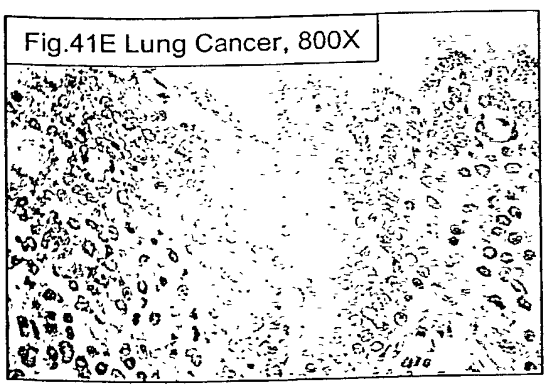


Fig.41E Lung Cancer, 800X

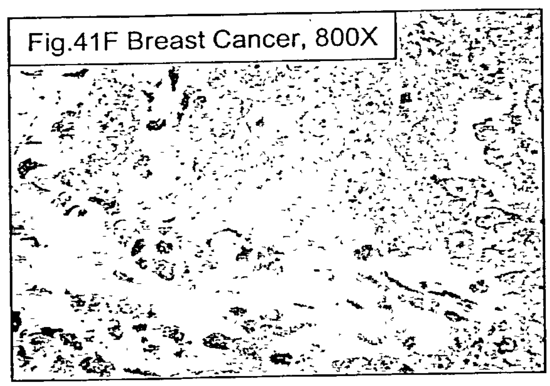


Fig.41F Breast Cancer, 800X

Figure 42

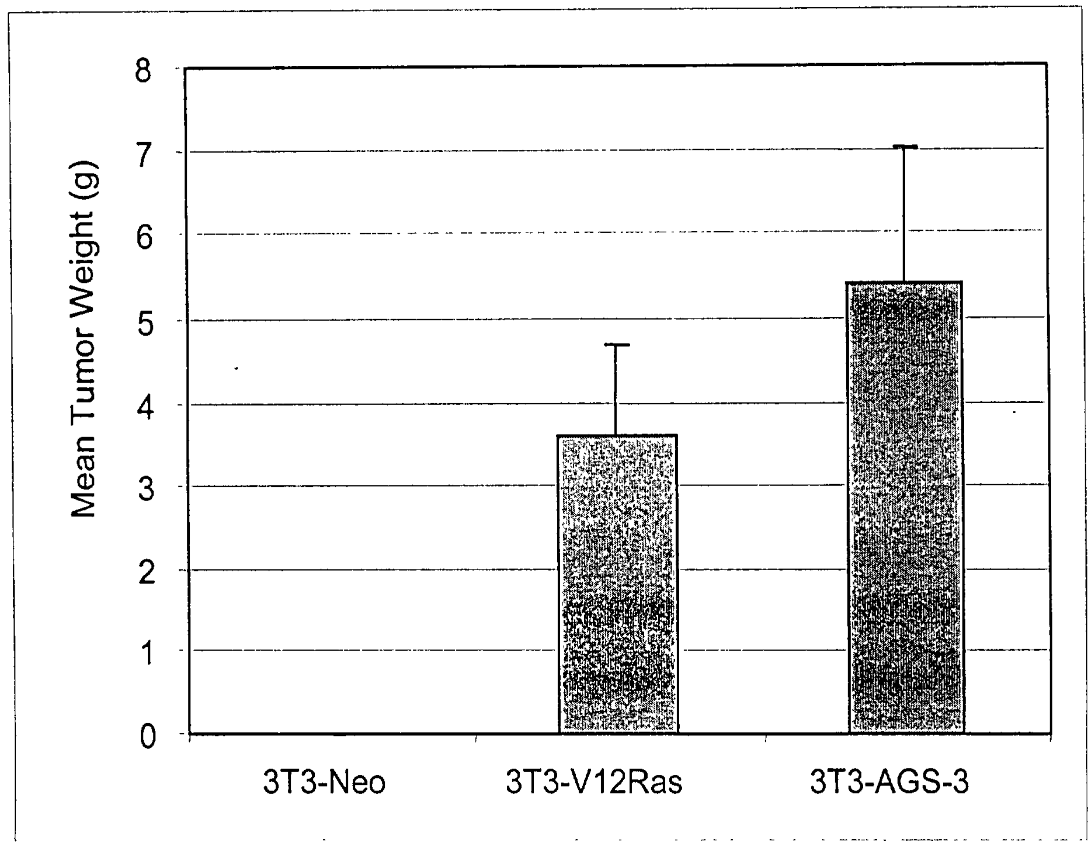
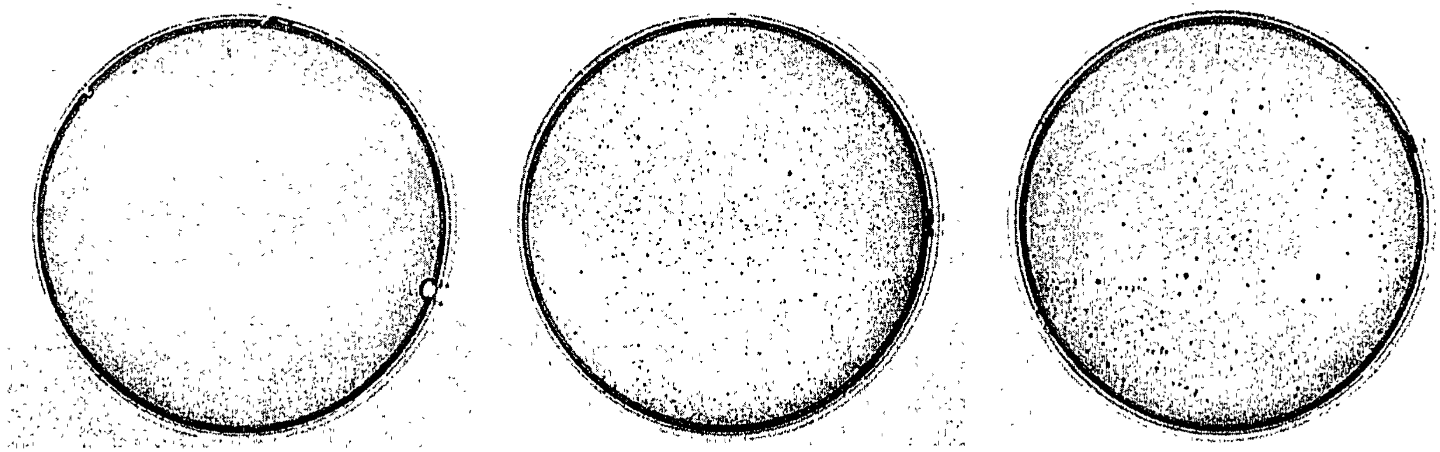


Figure 43



Neo 101P3A11 Ras

Cell Line	Colony number Average
3T3-neo	0.5
3T3-101P3A11	686
3T3-Ras	249